

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 19:06:21 ; Search time 516 Seconds
(without alignments)
5258.438 Million cell updates/sec

Title: US-10-044-205A-2
Perfect score: 2889
Sequence: 1 MVDGALDNLJANTAYIQAR.....NRPTGEGNSKSGVCLL 553

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.tmpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query *
No. Score Match Length DB ID Description

1	2889	100.0	1659	14	US-10-044-205A-3	Sequence 3, Appl1
2	2889	100.0	2198	14	US-10-044-205A-1	Sequence 1, Appl1
3	2883	99.8	1662	15	US-10-217-745-1	Sequence 1, Appl1
4	2883	99.8	1662	17	US-10-311-034-45	Sequence 45, Appl1
5	2883	99.8	1662	17	US-10-451-168-49	Sequence 49, Appl1
6	2883	99.8	2249	15	US-10-217-745-5	Sequence 5, Appl1
7	2876	99.6	1662	9	US-09-964-469-1	Sequence 1, Appl1
8	2876	99.6	1662	15	US-10-425-962-1	Sequence 1, Appl1
9	2823	97.7	1701	13	US-10-072-012-273	Sequence 273, Appl1
10	1801	62.3	1062	15	US-30-217-745-3	Sequence 3, Appl1
11	1528	52.9	36651	9	US-09-964-469-3	Sequence 3, Appl1
12	1528	52.9	36651	15	US-10-425-962-3	Sequence 3, Appl1
13	1283.5	44.4	1737	15	US-10-325-430-2	Sequence 2, Appl1
14	1283.5	44.4	2113	15	US-10-325-430-1	Sequence 2, Appl1
15	1252.5	43.4	2467	15	US-10-084-817-110	Sequence 110, Appl1
16	1252.5	43.4	2511	15	US-10-072-036-60	Sequence 60, Appl1
17	1252.5	43.4	2519	14	US-10-071-766-13	Sequence 13, Appl1
18	1252.5	43.4	2529	15	US-10-072-036-42	Sequence 42, Appl1
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22	1245.5	43.1	2519	10	US-09-971-392-72	Sequence 72, Appl1
23	1239	42.9	2848	16	US-09-873-367C-142	Sequence 142, Appl1
24	1239	42.9	2848	16	US-10-159-856-4	Sequence 4, Appl1
25	1235	42.7	2817	16	US-10-388-934-621	Sequence 621, Appl1
26	1233	42.7	2848	9	US-09-851-686-2	Sequence 2, Appl1
27	1226.5	42.5	2557	9	US-09-851-686-1	Sequence 1, Appl1
28	751.5	26.0	3527	16	US-10-062-674-1935	Sequence 1935, Appl1
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30	725.5	25.1	2362	16	US-10-117-722-273	Sequence 273, Appl1
31	722.5	25.0	2067	15	US-10-038-010-49	Sequence 49, Appl1
32	721.5	25.0	2067	16	US-10-305-720-1306	Sequence 1306, Appl1
33	701	24.3	2070	15	US-10-038-010-47	Sequence 47, Appl1
34	701	24.3	2683	12	US-10-152-319A-1539	Sequence 1539, Appl1
35	701	24.3	3283	16	US-10-191-803-38	Sequence 38, Appl1
36	701	24.3	3283	15	US-10-247-671-3	Sequence 3, Appl1
37	670	23.2	3154	10	US-09-955-999-45	Sequence 45, Appl1
38	663.5	23.0	1411	10	US-09-955-999-14	Sequence 14, Appl1
39	652.5	22.6	2037	13	US-10-087-684-23	Sequence 23, Appl1
40	652.5	22.6	2037	13	US-10-218-779-23	Sequence 23, Appl1
41	652.5	22.6	3073	13	US-10-029-020-11	Sequence 11, Appl1
42	580.5	20.1	1377	16	US-10-264-049-482	Sequence 482, Appl1
43	540	18.7	1679	9	US-09-771-161A-25	Sequence 25, Appl1
44	512	17.7	1416	9	US-09-938-842A-2503	Sequence 2503, Appl1
45	512	17.7	1416	11	US-09-938-842A-2503	Sequence 2503, Appl1

ALIGNMENTS

RESULT 1
US-10-044-205A-3
Publication No. US20020123464A1
GENERAL INFORMATION:
APPLICANT: KABELIER-LIBERMAN, Rosana
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
TITLE OR INVENTION: Uses Thereof
FILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044, 205A
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/241,884
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,877
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1659
TYPE: DNA

ORGANISM: Homo sapiens
US-10-044-205a-3

Alignment Scores:
Pred. No.: 0 Length: 1659
Score: 2889.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-044-205a-3 (1-1659)

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QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTGGGACAGCAAGAGCTGCGAGCGGCGGCTAGCTGCTGCTGCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGAGGGCTGGCGGAGCTCCGCGAAGCTGTCCCTGAACCTTCCAGAGCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCAATGGTGGCGCTCTTCCGTGACCTTCCAGCCACAGCTCCACGCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 241 CGAAGGCGGCAACCTTCTTGAAGAGAGCTGCAAGAACTGGAGCTGGCGAGAGAGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGCCCTGCGAGGGCTGGTGGCACTTGTGCGAGTCCCTGCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCAGCACCTTCTTCCAGCGAGCGCTGGCGACCAAGTCCACAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAAGGAGAGTGGCTGCGAGTACGCTGGCGCAAGCTGAGGCGCATGCTTCTTGAAG 480
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DB 481 CAGCCCTTTAAGGATTTGTGACCGAGCGCTTCTTACGACAAAGTTTCTGAGTGAATC 540
QY 181 PheGluMetGlnProValSerAspLysTyraPheThrGluPheArgValLeuGlyLysGly 200
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QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyraAlaCysLys 220
DB 601 GGTTTGGGAGGTATGTCGCGTCCAGTGAAGAACTGCGAAGATGATGATGCTGTAAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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QY 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyraAlaPheGluSer 260
DB 721 GAATCTTGGAGAAAGGTGACGAGCCCTTTCATGCTCTCTGCGCTTATGCTTTGAGAGC 780
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QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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DB 1201 GAGATTCGAAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGATGATTAATTCACA 1260
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QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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RESULT 2
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15921, and 15418, Methods and Compositions of Human Protein
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1


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; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205a-1

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US-10-044-205a-2 (1-553) x US-10-044-205a-1 (1-2198)

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QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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QY 81 ArgIySaIaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyPro 100
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DB 711 GAAGAGGAGGTGGCTGCGAGTGCAGCTGCGCAAGGCTGAGGCCATGGCTTTCTTCA 770
QY 161 GlnProPheIyAspPheValThrSerAlaPheIyAspIySLeuGlnTrpIySLeu 180
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QY 181 PheGlnMetGlnProValSerAspIySLeuThrPheThrGlnPheArgValLeuGlnIy 200
DB 831 TTGAGATGCAACAGAGTGTCAAGACAGTCTTCACTGATGTCAGAGTCTGGGGAAGG 890
QY 201 GlyPheGlyGluValCySaIaValGlnValIySAsnThrGlyIySMeTyrAlaCyS 220
DB 891 GGTTCGGGAGATATGCGCTGCAAGTGAAGAAACCTGGGAAGTATGACTGTAAG 950
QY 221 LysLeuAspIySLeuIySLeuIySLeuIySLeuIySLeuIySLeuIySLeuIyS 240
DB 951 AAACGTGACAAAGACCGCTGAAGAAAGGTGCGAGAAAGTGGCTCTCTTGGAAAG 1010
QY 241 GlnIleLeuGlnIySValSerSerProPheIleValSerLeuAlaTyrAlaPheGln 260
DB 1011 GAATCTTGGAGAGGTGTCAGACCTTTCATTTCTCTGTGCTTATGCTTTGAGAG 1070
QY 261 LysThrIleLeuCySLeuValMetSerLeuMetAsnGlyIyAspLeuIySLeuIyS 280
DB 1071 AAGACCATCTCTGCTTGTGATGAGCTGATGAATGGGAGAACCTCAAGTTTCAATC 1130
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheIySerAlaGlnIle 300

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DB 1191 GCGTGTGGATGTGTCACCTTCATGAAGACCTGCGCATCTGATCGGACATGAAGCTT 1250
QY 321 AsnValLeuLeuAspIySLeuIySLeuIySLeuIySLeuIySLeuIySLeuIyS 1340
DB 1251 AATGCTTCTGGAGAGCCTGCGCATCTGAGATGATGATGATGATGATGATGATG 1310
QY 341 MetIySLeuIySLeuProIleThrGlnArgAlaGlyThrAsnGlyIySLeuIyS 1360
DB 1311 ATGAAGGAGTGGCAAGCCATCAACAGAGGCTGGAAACCAATGGTTTACATGGCT 1370
QY 361 IleLeuMetGlnIySValSerIySLeuIySLeuIySLeuIySLeuIySLeuIyS 1380
DB 1371 ATCTTATGAAGAAAGTGAATTTCTTATCTGTCGATGCTGCTTTCATGAGAGC 1430
QY 381 IleTyrGlnLeuValAlaGlyArgThrProPheIySAspIySLeuIySValSerIyS 1400
DB 1431 ATTATGAATGGTGTGTCGAGCAACCATTCAAAGATTAAGAGAAAGGTCTGATA 1490
QY 401 GlnAspLeuIySLeuArgThrLeuGlnAspGlnValIySLeuIySLeuIySLeu 1420
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DB 1671 CGCTGGAAGCTGCTTATTAAGAAACCTTTCAGAGGCTTCTTCAATGATTAAT 1730
QY 481 LysAspIleAlaGlnIySAspAspPheSerGlnValA-GGlyValGlnPheAspIyS 1500
DB 1731 AAGAGCATCGCTGAATTTGATGATTTCTGAGGCTTCCGAGGAGTGAATTTGAT 1790
QY 501 AspIySLeuPheIySAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGln 1520
DB 1791 GATTAAGAGTCTTCAAAACCTTTCAGAGGCTTCTTCAATGATGATGATGAT 1850
QY 521 IleIleGlnIySLeuPheGlnGlnIySLeuIySLeuIySLeuIySLeuIySLeu 1540
DB 1851 ATTATGAAGAGGAGTGTGAGGAACTGAATGAACCCCAAGACCTTCAAGGTTG 1910
QY 541 GlnGlnAsnSerIySLeuIySLeuIySLeuIySLeuIySLeuIySLeuIyS 1553
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RESULT 3
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wiljanowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-1

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-217-745-1 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaIleuGlnAlaArg 20
DB 1 ATGGTGGACATGGGGGCGCTGGAAACCTGATCGCAACCGCTTACCTCGAGGCCCG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCTCGGACTGGACAGCAAGAGCTGCGCGCGCGCTGAGCTGCGCTGCGCTGCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhelHisSerLeu 60
DB 121 GGGCTGCGAGGCGTGGCGGAGCTCGCGCAAGGTGTCTGAACTTCCACAGCCTGTG 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
DB 181 GAGGAGGAGCCCATGGTGGCGCGCTCTTCCGTGACTTCTTACCAAGTCCCACTGTC 240
QY 81 ArgValAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluPro 100
DB 241 CGCAAGCGCGCACTTCTTGAGAGCGTGCAGAACTGGAGCTGCGCAAGAGAGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGCGCGCTGCGAGGGGCTGTGGCCACTGTGCGAGTCCCTGCGCGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysGlyGlnAlaAlaThrThrGlu 140
DB 361 AACCCGAACTCTTCTTCAAGCAGCGCGTGGCGCAAGAGGCCAAGCCCAAGCCCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgValaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGCGAGTGGCTGCGAGTACCGCTGCGCAAGGCTGAGGCCATGCTTCTTCAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTAAAGATTTCGTGACCAAGCGCTTCTTACGACAAAGTTCTCGAGTGGAAATC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTGAGATGCAACCGAGTGCAGCAAGTCACTTCACTGAGTTCGAGTGTGGGAGAAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTTTGGGAGGTAATGTGCGCTGCGTCAAGTGAAGAAACCTGGAGAAAGTGAAGCTGTAAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
DB 661 AAACGTGACAAAGAACCGGCTGGAAGAAAGAGTGGCGCAAGAGATGCTCTCTTGAAGAAAG 720
QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
DB 721 GAATCTTGAGAAAGGTACGAGCCCTTTCATGCTCTGCGCTTAAGCTTGTGAAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisLe 280
DB 781 AAGAGCCATCTGCTGCTTGTCAAGACCTGAGTGAATGGGGGAGAACCTCAAGTTCACATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300

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DB 841 TACAAGTGGCAAGCGGTGGCTGGACATGAGCGGGGTATCTTTACTGGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyTLeValTyrAspAspMetLysProGlu 320
DB 901 GCGTGTGGAGTGTGACCTCCATGAATCGGATGCTATTCGGGACATGAAGAGCTGAG 960
QY 321 AsnValIleLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
DB 1081 ATCTTAATGAAAGGTAAGTATTCATCTGAGACTGGATGGTTCATGGGATGCGAC 1140
QY 361 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTTATGAATGTTCTCTGAGCAACACATTCMAAGATTACAGAGAAAGTCACTGAAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAATTCAGCATGATACTTCAACA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGATTTTGGACGCTCTTCTTGGCTTAAGAAACCAAGGCAACCTTAAGAA 1320
QY 441 SerArgGlnLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAGAAAGTCTATGATCCAGAAACATCATTTCTTTAAAGATCAACATTTCTT 1380
QY 461 ArgLeuGlnAlaGlyLeuIleGluProPheValProAspProSerValValIleAla 480
DB 1381 CGCCTGGAAGCTGCTTAATGAACCCCATTTTGTGCCAGACCTTCAAGTGTATATCC 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
DB 1441 AAGAGCATCGCTAAATGATATTTCTGAGGTTCGGGGAGTGAATTTGATACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlnGlu 520
DB 1501 GATTAAGCAATTTCTTAAAACTTTGGCAGAGTGTCTTCTTAAGCATGCGAGAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGlnGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATAGAAACGGGAGCTGTTTGAAGAACTGAATGACCCCAAGACCTACGGGTTGTAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGATTAATTCATCCAAAGTCTGGGTGTGTTTATTTG 1659

RESULT 4
US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAU, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROMSKY, Mark L.
; APPLICANT: AU-YOUNG, Danice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHARLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyrung Alina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi

```

APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Daniel B.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAFALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURUBALAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KAHN, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Valda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 45
LENGTH: 1662
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-311-034-45 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 1 ATGGTGAACATGGGAGCCCTGGACACACCTGATCCGACACACGCTTACCTCCAGCCCG 60
QY 21 LysProSerAspCysAspSerIlySgileuGlnArgArgIserSerLeuAlaLeuPro 40
DB 61 AAGCCTCGGACTGGGACACGAAAGCTGCGACGCGGCGGCGGAGCTGCTGGCCCTGCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuAlaGlnIlyLeuSerIleuAsnPhaIleuSerLeu 60
DB 121 GGGCTCGAGGGCTGGGCGGAGCTCCGCCAAGAGCTGTCCCTGAACCTTCACAGCCTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGGACGACCCATCGCTCCGCCCTCTTCCTGATCTTCTACCAACAGTCCCAAGCTTC 240
QY 81 ArgValAlaAlaIlePheLeuGluAspValGlnAsnIlePheGluLeuAlaGluGlnGlyPro 100
DB 241 CGAAGGCGGCACTCTTCTAGAGAGCTGCGAAGCTGGAGCTGGCCGAGAGAGGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

DB 301 ACCAAGAAGCGCGCTGCGAGGCGCTGGCCACTTGGCAAGTCCCTCCCGGCG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaIleThrLysCysGlnAlaIleThrGlu 140
DB 361 AACCCGCAACCTTCTTCCAGCCAGCCGCGTGGCCAGGAGCCAGGAGCCAGCCAGCTAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgValAlaGluAlaMetAlaPheLeuGlnIle 160
DB 421 GAAAGGAGAGTGGCTGACAGTACGCTGGCCAGAGGCTGAGGCCATGGCTTCTTCCAGAG 480
QY 161 GlnProPheLysAspPheValIleThrSerAlaPheTyrAspLysPheLeuGlnIlePhe 180
DB 481 CAGCCCTTAAAGATTGCTGACAGGCGCTTCTACGCAAGATTCTCGAGTGGAACTCC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlnLysGly 200
DB 541 TTGGAGATGCAACCACTGTCAGACAGTACTTCACTGATCAAGTGGAGTGGGAGAAAGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
DB 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAACACTGGAAAGATGATGCTGTAG 660
QY 221 LysLeuAspLysIlyArgLeuLysLysGlyGlyGlyIleValMetAlaLeuLeuGlnLys 240
DB 661 AAACCTGACAAAGAGCGGCTGAGAGAAAGGTGGCGAAGATGGCTCTTGGAAAAAG 720
QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
DB 721 GAATCTTGGAGAGGTGACAGAGCCCTTTCATTGCTCTCTGGCTTATGCTTTAGAGC 780
QY 261 LysThrIleLysCysLeuValMetSerLeuMetAsnGlyLysPheLysPheIle 280
DB 781 AAGACCATCTCTGCTTCTTCTCATGAGCTGTATGATGAGGAGAGCTCAAGTTCCATC 840
QY 281 TyrAsnValAlaGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
DB 841 TACAACTGGGCGAGGCTGACATGAGCGGATGATCTTAACTCGGCCCAAGATA 900
QY 301 AlaCysGlyMetLeuIleSerLeuGlnIleValTyrArgAspMetLysProGlu 320
DB 901 GCTGTGGAGTGTGCACTCTCAAGAACTGGCATGCTTATGGGACATGAAGCTTAG 960
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlnAlaValGlu 340
DB 961 AATGCTCTTGGATGACCTCGGCACTGCAAGGTTATCTGACTGGGCGTGGCGTGGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
DB 1021 ATGAAGGTTGGCAAGCCCATCAAGAGGCTGGAAACAAATGATTACATGCTCTTAG 1080
QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTTAATGAAAGGTAAGTATTCCTATCTTGGACGTGTTTCCATGGAGATGACG 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrIlySgileuValSerLys 400
DB 1141 ATTATATGAATGGTCTTGGACGAACCATTCMAAGATTACAAGGAAAGGTGCTGATAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnIleAspAsnPheThr 420
DB 1201 GAGGATCTGAAGCAAGAACTCTCAAGAGAGGTCAAATTCAGATATATTAACCTTCA 1260
QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAGCAAAAGATTTTGGAGGCTTCTTGGCTTAAGAAACAGAGCAAGCTTAGA 1320
QY 441 SerArgLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPhePro 460
DB 1321 AGCAGAAAGAGCTGATGATCCAGGAAACATCTTCTTAAACGATCACTTCCCT 1380
QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerAlaValTyrAla 480
DB 1381 GCGCTGGAAGCTGGCTAATTAAGAACCCCATTTGGCCAGACCCCTTCAAGTGGTTATGCC 1440

QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAGACATCGCTGAATGATGATTTCTCTGAGTGGGGGTGGATTTGATGACAA 1500
QY 501 AsplgslNphePheLysAspPheAlaThrGlyAlaValProIleAtrPglngluGlu 520
Db 1501 GATAGCAGTCTTAAATACTTTGGCAGAGTGTCTTCTATAGCATGGCAGAAAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATGAACCGGACGTTTGGAGAACGATATACCCCAACAGACTTACGGGTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
Db 1621 GAGGTATTCATCCAMGCTGGCGTGTGTGTATTG 1659
RESULT 5
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49
Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0
US-10-044-205a-2 (1-553) x US-10-451-168-49 (1-1662)

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGACAGGGCTGCGCGAGCTCCGCCAGAGCTGTCCCTGAACCTTCCACAGCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGAGCCCATCGGTGCGCGCTCTCCGTGACTTCTACGACAGAGCCCAAGTTC 240
QY 81 ArgGlyAlaAlaThrPheLeuGlnAspValGlnAsnTPGluLeuAlaGluGluPro 100
Db 241 CGCAAGGGCGCAACTTCTTAGAGAGAGTGCAGAACGAGGAGTGGCCAGAGGAGACC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCCCGCTGAGGGGCTGTGGCCACTTGTGGATGTGCCCTCGCCCGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrGlu 140
Db 361 AACCCGACACCTTCTCCTCAGCCAGGCGGTGGCCACCAAGTCCCAAGCCAGCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
Db 421 GAAGAGCGAGTGCCTGACGTGACCTGGCCAGAGCTGAGCCATGAGCTTCTTGGAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyraAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGATTTCTGTGACAGCGCTTCTACGACAGATTTCTGACAGGAAATC 540
QY 181 PheGluMetGlnProValSerAspLysTyraPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TCGAGATGCAACAGTGCAGACAGACTTCACTGAGTTCAAGAGTGGCGGAAAGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyraLysLys 220
Db 601 GATTGTGGAGGATATGTCGCTCCAGGTGAAACACTGGGAAAGATGATGCTGTAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
Db 661 AATCGGACAGAGAGCGCTGAGAGAGAAAGATGCGGAGAGATGCTCTTGGAGAAAG 720
QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyraAlaPheGluSer 260
Db 721 GAATCTTGGAGAGAGTCCAGAGCGCTTTCATGTCCTCTGGCGCTTATGCTTAAAGGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyValAspLeuLysPheHisIle 280
Db 781 AAGACCATCTCTGCTGTGTATGATGCTGTATGAGGGGAGACCTCAAGTTTCCATTC 840
QY 281 TyraAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyraSerAlaGlnIle 300
Db 841 TACAACTGGGAGCGGTGGCTGGAGATGAGCGGGGTGATCTTTTACTGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyraGlnPheMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCATGAACTCGGCATCGTCTATGCGGACAGAGAGCTTAG 960
QY 321 AsnValLeuLeuAspSerLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 961 AATGTGCTTCGATATACCTCGGCACTGAGAGTTATCTGACCTCGGGGCTGGCCGTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyraMetAlaProGlu 360
Db 1021 ATGAAAGGTGGCAAGGCCATCACCCAGAGGGCTGGAAACCAATGTTTCACTGCTCTGAG 1080
QY 361 IleLeuMetGlyLysValSerTyraSerTyraProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGAAGAAAGGTATGATTTCTATCTGAGACTGTGCACTGTGCAAGGATGAGC 1140
QY 381 IleTyraMetValAlaGlyArgThrProPheLysAspTyraLysGluLysValSerLys 400
Db 1141 ATTATGAATGTTCTCTGAGAGACACCATTCAAAGATTTACAGAGAAAGGTCAAGTAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

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Db      1201 GAGGATCTGAAACAAAGAACTCGCAAGACGAGGTCAAAATTCACACATGATTAATTCACAA
Qy      421  GUGUUAUAlayAspIleCyArGleuPheleuAlaySlyProGluGlnAryLeuGly  440
Db      1261 GAGGAGCAAAAGATATTTGTCAGGCTCTTTGCTTAAGAAACGAGACAAAGCTTAAAGAA
Qy      441  SerArgGluLySerAspAspProArgLyShiSphPheLysThrIleasnPhePro  460
Db      1321 AGCAGAGAAAGTGTGATGATCCAGAAACATCATTTCTTTAAACATCAATTCCT
Qy      461  ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla  480
Db      1361 CGCTGGAAGCTGGCTGAATTTGAACCCCATTTGTGCCAACCCCTTCAGTGCTTATGCC
Qy      481  LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys  500
Db      1441 AAAAGACATCGCTGAATTTGATGATTTCTCTGAGGTTGCGGGGGTGGAAATTGATGACAA
Qy      501  AspLysGlnPhePheLysAspPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu  520
Db      1501 GATAGCAGTCTTCTCAAAAATTGTCGACAGGTGCTGTCTTATGATGGACGAGAAAGA
Qy      521  IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu  540
Db      1561 ATTATGAAACGGGACTGTTTGAAGAACTGATGACCCCAACGACACTACGGGTGTGAG
Qy      541  GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu  553
Db      1621 GAGGTTAATTCATCCAAAGTCTGGCGTGTGTTTGTATTG  1659

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RESULT 6

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US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

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Alignment Scores:

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Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

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US-10-044-205A-2 (1-553) X US-10-217-745-5 (1-2249)

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Qy      1  MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg  20
Db      354  ATGATGACATGGGGGCTTGGAACCTGATCCCAACCGCTTACCTGCAAGCCCG  413
Qy      21  LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro  40
Db      414  AAGCCCTCGGACTGGACGACAAAGCTGCAAGCGCGGCGGCGGATGCTTGGCTTGGCCCTGCCC  473

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Qy      41  GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys  60
Db      474  GGGCTGCAAGGGCTGCGCGGAGACTCCGCAAGAGCTGTGCTTCAATTCACAGCTGTGTG  533
Qy      61  GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe  80
Db      534  GAGGAGAGGCGCATGCTGCTGCGGCTCTTCGATGATCTTCAGACAAATGCGCCAGCTTC  593
Qy      81  ArgLysAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluIlePro  100
Db      594  CGCAAGCGGCAACCTTCTTCAAGAGAGCTGCAAGACTGGAGACTGGCCGACGAGAGGAGCC  653
Qy      101  ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly  120
Db      654  ACCAAAGACAGCGCGCTGCAAGGCGCTGTGTGCACTTGTGCAAGTGTGCGCCCTGCGGAG  713
Qy      121  AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu  140
Db      714  AACCCGCAACCTTCTCTCAAGCAGGCGGTGGCCACAAAGTCCAAAGCAGCAGCAGCTGAG  773
Qy      141  GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu  160
Db      774  GAAAGCGAGTGGCTGCAAGTGAACCTGCGCAAGCTGAGGCGCATGCTTCTTGGCAAGAG  833
Qy      161  GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu  180
Db      834  CAGCCCTTTAAGGATTTGCTGACCAAGGCTTCTCAAGCAAGTTCTTGGACGTGGAACCTC  893
Qy      181  PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGluLysGly  200
Db      894  TTGAGAGATGCAACAGTGTCAAGCAAGTACTCAGTGTGCAAGTGTGCGGGGAAAGT  953
Qy      201  GlyPheGlyGluValCysAlaValAlaGlnValLysAsnThrGlyLysMetTyrAlaCysLys  220
Db      954  GGTTTTGGGAGGATATGTCCTGCTCAAGTGAAGAAACATCGGAAAGATGATGCTGTAG  1013
Qy      221  LysLeuAspLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys  240
Db      1014  AAACGTGCAACAAAGAGGCGCTGAAGAAAGGTGGCGAAGATGCGCTCTTGGAAAG  1073
Qy      241  GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer  260
Db      1074  GAAATCTTGGAGAGAGGTCAAGAGCCCTTCAATGCTCTCGGCGCATGCTTGAAGAGC  1133
Qy      261  LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle  280
Db      1134  AAGACCATCTTCTGCTGCTGTGATGAGCTGATGAAATGGGGAGACCTCAAGTTCACATC  1193
Qy      281  TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle  300
Db      1194  TCAACCTGGGCGAGCGGTGGCTGGAATGAGCCGGGTGATCTTTACTGCGCCAGATA  1253
Qy      301  AlaCysGlyMetLeuHisIleHisGluLeuGlyIleValTyrArgAspMetLysProGlu  320
Db      1254  GCGTGTGAGATGTGACCTTCATGAACCTGGAATCGGATCGTATTCGGAACATGAAGCTTAG  1313
Qy      321  AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu  340
Db      1314  AATGCTCTTGTGATGACCTCGCAACTGAGGTTATCTGACCTGGGGCTGGCCGTGAG  1373
Qy      341  MetLysGlyIleLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu  360
Db      1374  ATGAAGGATGGCAAGCCCATCAACCAAGGGCTGGAACCAATGATTAATGCTGCTTAG  1433
Qy      361  IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer  380
Db      1434  ATCTTAATGGAAGAGTAAATTAATTCATCTGAGACCTGTTTGCATGGAGGATGAGC  1493
Qy      381  IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys  400
Db      1494  ATTTATGAAATGTTGCTGCAAGCAACCATTCAAAGTTTCAAGAGAAAGGTCTGTTAA  1553
Qy      401  GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr  420

```


Db 1201 GAGGATCTGAAGCAAAAGACTGACAGAGGCTCAAAATTCACAGATGAATCACTTCACA 1260
 QY 421 GUGUUAUAlaAspIleCysArgLeuPheLeuAlaIleValProGluGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATATTCAGAGCTCTTCCTGGCTTAAGAAACGAGAACCTTGA 1320
 QY 441 SerArgGluValSerAspAspProArgIleHisIlePhePheValThrIleAsnPro 460
 Db 1321 AGCAGAGAAAGAGCTGATGATCCAGAGAAACATCATTTCTTAAAGATCACTTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValIleAla 480
 Db 1381 CGCTGGAGAGCTGGCTTAATGAGACCCCATTTTGGACAGACCTTCAGAGGTTATG 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgIleValGluPheAspAsp 500
 Db 1441 AAGACATCTGCTGAATTAATGATTTCTCTGAGGTTGGAGGAGTGAATTTGATGACA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1501 GATAGCAAGTCTTCATAAACTTGTGACAGAGTCTGTTCTATAGCATGGCAGAGAA 1560
 QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATGAAACGAGACTGTTTGAGAGACTGATGACCCCAACAGACCTTACGAGTGTG 1620
 QY 541 GlnGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 Db 1621 GAGGTAATCATCTCAAGCTGGCGTGTGTTGTTATTTG 1659

RESULT 8

US-10-425-962-1
 ; Sequence 1, Application US/10425962
 ; Publication No. US20030180786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: C1000634D102
 ; CURRENT APPLICATION NUMBER: US/10/425,962
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: 09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-425-962-1

Alignment Scores:

Pred. No.: 0 Length: 1662
 Score: 2876.00 Matches: 551
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 2
 Query Match: 99.55% Indels: 0
 DB: 15 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-425-962-1 (1-1662).

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGTGACATATGAGGAGGCTGACCAACTGATCGCCACACGCGCTTACCTGACGAGCCGG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

Db 61 AAGCCCTCGGACTGCGACAGCAAAAGCTGACGCGGCGCGCTGAGCCCTGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheIleSerLeuCys 60
 Db 121 GGGCTGAGGGGCTGCGGAGAGCTCCCGAGAGCTGTCTGAACTTCCAGAGCTGTGT 180
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGAGCCCATGCGTGGCGGCTCTTCGCTGACTTCCAGCCACAGTGGCCACGCTTC 240
 QY 81 ArgIleAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
 Db 241 CGCAAGCGGCAACCTTCTTAAGAGAGCGTGCAAGCTGGAGCTGGCTCAGAGAGGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAACACGCGCGCTGAGAGGCTGTGGCTCACTTGTGAGTGTCCCTGCCCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCCTGCAACCTTCTCAGCCAGGCGGCGGCAACAGAGTGCACACAGCCACCTGAG 420
 QY 141 GlnGluArgValAlaAlaValThrLeuArgIleAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAAGAGGAGGTGCTGAGTACGCTGGCAAGGCTGAGGCAATGCTTCTTTCAGAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTAAAGATTTGTGTACACGCGCTTCTACAGCAAGTTTCTGAGAGGAACTC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 541 TTCAGAGTGCACACAGTGTGACAGAACTTCACTGAGTTGAGATGTGCGGAGAAAGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGAGAGTATGTGCGCTCCAGTGAGAAACACTGGAGAAATGTATGCTCTGTAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGlyLys 240
 Db 661 AAACCTGCAACAAAGAGCGCTGAAAGAAAGTGGCCAGAAAGTGGCTCTCTGGAAAG 720
 QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAATCTTGGAGAAAGTCAAGAGCCCTTCATTGTCTCTGCGCTATGCTCTTGAAGAC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyLysPheIleGlyLe 280
 Db 781 AAGACCCATCTGCGCTGTATGATGAGCTGATGAATGGGAGAACTTCAGATCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACAACTGGGAGACCGCGGCTGTGACATGAGCCGGGATCTTTTACTCGGCCCAAGTA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCGTGTGAGATCTGCACCTCATGAACCTCGGCACTGCTATGCGGACATGAAGCCCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGlu 340
 Db 961 AATGTGCTTGTGATGACCTTGCACTGCACTGAGTTATGTACCTGGAGGCTGGCGTGAAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGAGTGGCAAGCCCATCAACAGAGGCTGGAACCATGGTTTACATGCTCTGAG 1080
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGGGAAAGATATGATATCTTATCTTGTGAGCTGGGTTTGCATGGAGATGACG 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTATGAATGTGTTGCTGAGAGAAACATTCATCAAGATTTCAGAGAAAGATGATGAA 1200

QY 401 GluAspLeuGlnArgThrLeuGlnAspGluValIysPheGlnHisAspAspPheThr 420
DB 1201 GAGGATCTTAAAGCAAGAAAGCTGCGAAGCGAGGCAAAATTCAGATGATTAATCTTACA 1260
QY 421 GluGluValIysAspLeuIleCysArgLeuPheLeuValIysPheGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGATTTGAGGCTCTTCTGGCTAAGAAACGAGACAAAGCTTAAGA 1320
QY 441 SerArgGluLysSerAspAspProArgGlyShiShiSphPheLysThrIleAsnPro 460
DB 1321 AGCAGGAAAGTCTGATGATCCAGAGAAACATATTTCTTAAACATCACTTCCCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValIleAla 480
DB 1381 CGCCTGGAAGCTGCGCTTAATTGAAACCCCATTTGTCCAGACCCCTTCAGTGTATGCC 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgIleValGluPheAspAspLys 500
DB 1441 AAAGACATCGTGAATGATGATTTCTCTGAGGTCGAGGAGTGGAAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaIlePheGlnGlu 520
DB 1501 GATPACCAATGTTCTTCAAAAATTGCGACAGTCTCTTCTTAATGACATGCGAAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATATAGAAACCGGACCTGTTTGAGAACTGAAATACCCCAACGACCTACGGGTGTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
DB 1621 GAGGTAATTCATCCAAAGTCTGAGCTGTGTGTTATTG 1659

RESULT 9

US-10-072-012-273

Sequence 273, Application US/10072012

Publication No. US2004003493A1

GENERAL INFORMATION:

APPLICANT: Tchernyev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patuturajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esna
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 273
LENGTH: 1701
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-012-273

Alignment Scores:
Pred. No.: 0 Length: 1701
Score: 2823.50 Matches: 547
Percent Similarity: 98.568 Conservative: 0
Best Local Similarity: 98.568 Mismatches: 1
Query Match: 97.738 Indels: 7
DB: 13 Gaps: 3

US-10-044-205a-2 (1-553) x US-10-072-012-273 (1-1701)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 19 ATGTGGACATGGAGGAGCCCTTGACACACTGATGCGCAACAGCTTCACTTGAGAGCCGG 78
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaPro 40
DB 79 AAGCCTCGAGTGGAGAGCAAGAGAGCTGAGCGCGCGGCGTGGCCCTGCGCC 138
QY 41 GlyLeuGlnIleCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 139 GGGCTGAGGGGCTGGCGGAGCTCCGCGAGAGCTGCTCCGAACTTCCACAGCTGTGT 198
QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 199 GAGCAGAGCCCATGCGTCCGCGCTTCTTCCGCTTCCAGCAGAGTCCAGCTTC 238
QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGlnGluIlePro 100
DB 259 CGCAAGCGGCAACCTTCTCTAGAGAGAGTGAAGACTGGAGCTGGCGAGGAGGAGCC 318
QY 101 ThrLysAspSerLysLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 319 ACCAAAGACGCGCGCTGACAGGGGCTGGGCACTTGTGAGATGCCCTTCCCGGGG 378
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrGlu 140
DB 379 AACCCGAAACCTTCTCTACGACGAGCCGTGGCCACCAAGTCCACAGACCACTGAG 438
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
DB 439 GAAAGCGAGTGGCTGAGTACGCTGGCCAAAGCTGAGGCGTGTCTTCTTCAAGAG 498
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 499 CAGCCCTTAAGGATTTGTATCCAGCGGCTTCTTCAAGATTTCTTGAAGTGAAGCTC 558
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
DB 559 TTCAAGATGCAACAGTGTGACAGCACTTCACTGATGTTCAAGTGTGAGGAGAAAGT 618
QY 201 GlyPheGlyGluValCysAlaValAlaGlnValIleAsnThrGlyLysMetTyrAlaCysLys 220

Publication No. US20030004328A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
TITLE OF INVENTION: Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/10/217,745
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1062
TYPE: DNA
ORGANISM: homo sapiens
US-10-217-745-3

Alignment Scores:
Pred. No.: 2,44e-215 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: Gaps: 0

US-10-044-205A-2 (1-553) x US-10-217-745-3 (1-1062)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ArgGtGACATGGGGGCTCGAGACACTGATGCCACACCGGCTTCTCGACGGCCCG 60
QY 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCTCGACCTGCACACGAAAGAGCTGCACGGCGGGCGGAGCCTGGCCCTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGACAGGGCTGCGCGGAGCTCGGCACAAAGCTCTCCCTGAACCTCCACACCTGT 180
QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrAlaProThrPhe 80
Db 181 GAGCGACAGGCCATCGGTCGCCGCTCTCCGAGACTTCTTACGACAGTGGCCACGTTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyPro 100
Db 241 CGCAAGCGGCGAACCTTCTTACAGSACGTGCACAAATCGGAGAGCTGGCGAGGAGACC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGCGAGGGGCTGGTGGCCACTTGGCGAGTGGCCCTCGCCGGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140
Db 361 AACCCGCAACCTCTCTCAGCCAGGCGGTGGCCACCAAGTGGCAAGACCCACCATGAG 420
QY 141 GlnGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGln 160
Db 421 GAAAGCGACAGTGGCTGCAGTACGCTGGCCCAAGGCTGAAGGCGCTTCTTGGCAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTAAAGATTTCGTGACCAAGCCCTCTTACAGCAAGATTTCTGCAAGTGAATCC 540
QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlnLysGly 200
Db 541 TTCGAGAGCAACCAAGTGCAGACAAAGTACTTCACTGAAGTTCAGAGTGGGAGAGGT 600
QY 201 GlyPheGlyGlnValCysAlaValGlnAlaLysAsnThrGlyLysMetTyrAlaCysLys 220

Db 601 GGTITGGGGAGTATGTCCTTCACAGTGAACCACTGGAGATGATGCTGTAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
 Db 661 AAATGGACAAAGACCGCTGAAAGAGAGGTGGCCAGAGAGATGCTCTCTGGAAAG 720
 QY 241 GlnLysLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAAATCTTGAGAGAGTACAGACCTTCCTCATTTGCTCTGCGCTGAGGCTTTGAGAG 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetLysGlyLysAspLeuLysPheHisIle 280
 Db 781 AAGACCATCTCTGCTTGTTCATGACCTCGAGATGAGGAGAGACCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACACGTGGGACCCGCTGGCTGGACATGAGCCGGTGTCTTTTACTCGACCGAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyrArgAspMetLysProGln 320
 Db 901 GCGTGGGATGCTGCACCTTCACATGAACTCGGCATCGCTATCGGAGATGAGCCGTAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyLysAsnCysArgLeuSerAspLeuGlyLeuAlaValGln 340
 Db 961 AATGTCCTTCTGAGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCTGGCTGGAG 1020
 QY 341 MetLysGlyLysLysProIleThrGlnArg 350
 Db 1021 ATGAAAGGTGGCAAGCCCATCACCCAGAG 1050

RESULT 11

US-09-964-469-3
 ; Sequence 3, Application US/09964469
 ; Patent No. US20020034803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CT000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-964-469-3

Alignment Scores:

Pred. No.: 1,32e-178 Length: 36651
 Score: 1528.00 Matches: 349
 Percent Similarity: 41.40% Conservative: 0
 Best Local Similarity: 41.40% Mismatches: 1
 Query Match: 52.89% Indels: 493
 Db: 9 Gaps: 1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 2076 ATGCTGGACATGGGGGCGCTTGACACACTGATGCGCAACACCGCTTACTGCGAGCGCG 2135
 QY 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40

Db 2136 AAGCCCTCGACCTGCGACAGCAAGAGACTGACGCGCGCGCTTACCTGCGCTGCC 2195
 QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 2196 GGGCTGCAAGGCGCTGCGCGGAGCTCGGCAGAGACTGCTCCGAACTTCCACAGCTGTGT 2255
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValIleProThrPhe 80
 Db 2256 GAGCAGAGCCCATCGGTGCGCGCTTCTTCGAGACTTCTTACGACAGAGGCGCGCTTC 2315
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTyrGlnLeuAlaGlnGlnIlePro 100
 Db 2316 CGCAAGGGCGCAACCTTCTCTAGAGAGAGTGGAGACTGGAGCTGGCCAGAGAGAGAGCC 2375
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 2376 ACCAAAGACAGCGCGCTGCGAGGCGCTGTGCGCACCTTGTGCGAGTGCCTCGCGGG 2435
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140
 Db 2436 AACCGCAACCTTCTCTGAGCAGGCGGTGGCCAGAGTCCAGAGCGACACCTAG 2495
 QY 141 GlnGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGln 160
 Db 2496 GAAAGCGAGTGGCTGCGAGTACCGCTGCGCAAGGCTGAGGCGCAAGGCTTCTTGCAGAG 2555
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 2556 CAGCCCTTTAAGGATTTGCTGACAGCGCGCTTCTTACGAAAGTTTCTGCGAGGAAATC 2615
 QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
 Db 2616 TTCCAGATGCAACCGTGTGACAGCAATCTTCACTGAGTTCAAGATGCTGGGGAAGGT 2675
 QY 201 GlyPheGlyLys 204
 Db 2676 GGTITTTGGAGGTAAAGTGTCCAGTAGCAGGCTGAAGGTGAAGCATAGAGCATGA 2735
 QY 204 204
 Db 2736 AAGGGGTAATGTCCTTCTTTTAAATCGATTAAGTAATTCAGAC 2795
 QY 204 204
 Db 2796 CATATGAGAGATTTCTAGCCCGGTCTCCAGCCCTTCTTTGTGTGCCATGTGTG 2855
 QY 204 204
 Db 2856 TGAATTAACCAACAAATGCGATGAGAGAGCAAGCAAAATTTATCTTGGCAAGACTCT 2915
 QY 204 204
 Db 2916 GTCATGGGTCTCATTAAGAACTGTGATGATGCTGACACTTCAGAGATGATAGCAA 2975
 QY 204 204
 Db 2976 TGTGTGACAGAGATCTCCGTTCCCTTAATTGTGATTAAGAGCACTTAAGAAAAA 3035
 QY 204 204
 Db 3036 TGTATATTTAAGAAATATCTTAATAGCTGGGTGTGTGTGACATGCTGTATCCAGCT 3095
 QY 204 204
 Db 3096 ACTTGGAGGCTGAAGCAGAGAGATCATTTAGCTGGAGGTGAGAGTTGCAGTAGGCC 3155
 QY 204 204
 Db 3156 AAGATGTGTGCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAA 3215
 QY 204 204

QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 Db 2256 GAGAGAGACCCATGGGTGGCCGCTCTTCGTGATCTTCTTACCGACAGTCCACGCTTC 2315
 QY 81 ArgGlyAlaAlaThrPheLeuGluAspValGlnAsnTrpGluAlaGluGluPro 100
 Db 2316 CGCAAGCGCGCAACCTTCTCTAGAGACGTGCAGAACTGGAGCTGGCGAGAGAGGACC 2375
 QY 101 ThrIleAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 2376 ACCAAGACAGCGCGCTGCAGGGGCTGTGGCCACTTGTGCAGGTGCCCCGCGGG 2435
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrIleCysGlnAlaAlaThrThrGlu 140
 Db 2436 AACCCGCAACCTTCTCTCAGCGCGCGGTGGCCAAAGGCCAAGCCACACGCTGAG 2495
 QY 141 GluGluArgValAlaAlaValAlaThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 2496 GAAGAGCGAGGTGGCTGCAGTGCAGTGCAGGCTGAGGCTGAGGCTTCTTGCAGAGG 2555
 QY 161 GlnProPheIleAspPheValThrSerAlaPheTrpAspIlePheLeuGlnTrpLysLeu 180
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 QY 204 ----- 204
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 QY 204 ----- 204
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 QY 204 ----- 204
 Db 3516 TTTCGTCTAGGATTTGCTATTTCTGGGTGTTTCAACAATATGTGACCTTTGTGT 3575
 QY 204 ----- 204
 Db 3576 CTGGCTCTTTCACCTAATTAAGATTTTGGGGTTCATTGCACAGTAGATGTGCA 3635
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 QY 204 ----- 204
 Db 3696 TAGCAATTCATCTGTGATGACACTTGGGCTGTTTCACTTTGGCTATGTGTATGG 3755
 QY 204 ----- 204
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 QY 204 ----- 204
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 QY 204 ----- 204
 Db 3876 CCAAACTTCACATTTTATTTCCACAGCAATCTTAAGSTTTCGATTTCTCCACA 3935
 QY 204 ----- 204
 Db 3936 TCCTTGCAACAATGATATTTTCTGTATTTTATTAAGAGCTGCTAGTAGGTGA 3995
 QY 204 ----- 204
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 QY 204 ----- 204
 Db 4056 CTTTCTCAATGCTTAACATCTTTCCACCACTCTCTTATATCATCTCACTCTCTG 4115
 QY 205 ----- ValCysAlaIle 208
 Db 4116 CAGTACCATCACTTCACTCTTTCTCTCTCTTTCTCTCTTAAAGATATGCGGT 4175
 QY 208 IglValIleAsnThrGlyLysMetIleValCysIleLysLeuAspLysIleValArgLeu 228
 Db 4176 CCAAGTAAAAACAATCGGAGAGATGATGCTCTTAAGAACTGAGCAAAAGCGGCTGAA 4235
 QY 228 sLysLysGlyGlyLysMetAlaLeuLeuGlnIleLeuGlnLysValSer 248
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 QY 288 uAspMetSerArgValIlePheTrpSerAlaGlnIleAlaCysGlyMetLeuHisLeu 308

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Db      4416 GGCATGAGCCGGGTGATCTTTTACTGCGCCAGATAGCCCTGTGGAGTNGCTGCACCTCCA 4475
Qy      308 sglueuglyllevaityrargaspmetlvsProgluamValleuenuaspplengl 328
Db      4476 TGAAGTCGATCTCTTATCGGACATAGACCTGAGATGCTCTTGCATACCTCG 4555
Qy      328 yAnCysargleuSeraspplenglYleuAlaValgluMetlvsGlylyAspProleth 348
Db      4536 CAAGTCAGAGTTATCTGACCTGGGGCTGCGCGTAGATGAGAGGGGTGGCAAGCCATCAC 4595
Qy      348 rglNArg 350
Db      4596 CCAGAGG 4602

RESULT 13
US-10-325-430-2
/ Sequence 2, Application US/10325430
/ Publication No. US20030153525A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc
/ APPLICANT: Siles-Santiago, Imaculada
/ APPLICANT: Rosenfeld, Julie Beth
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
/ FILE REFERENCE: MP101-294P1RNM
/ CURRENT APPLICATION NUMBER: US/10/325,430
/ PRIOR FILING DATE: 2002-12-19
/ PRIOR APPLICATION NUMBER: US 60/341,953
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1737
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1737)
US-10-325-430-2

Alignment Scores:
Pred. No.: 4.67e-150 Length: 1737
Score: 1283.50 Matches: 255
Percent Similarity: 65.49% Conservative: 96
Best Local Similarity: 47.57% Mismatches: 162
Query Match: 44.43% Indels: 23
DB: 15 Gaps: 8

US-10-044-205A-2 (1-553) x US-10-325-430-2 (1-1737)
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Qy      46 AlaGluLeuArgGlnLysLeuSerleuAsnHehIsSerLeuCysGlnGlnGlnProIle 65
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Qy      66 GlyArgArgleuPheArgAspPheleuAlaThrValProThrPheArglyAlaAlaThr 85
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Qy      PheLeuGluAspValGlnAsnThrGluLeuAlaGluGlyProThrLysAsp----- 103
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Qy      143 ArgValAlaAlaValThrLeuArgLysAla-----GlnAlaMetAla 156
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Db      817 AAGTTTACATTTTAAACCTGGGCAATCCCGCTTTATATAGAGAGACCGGTTTCTAT 876
Qy      297 SerAlaGlnAlaAlaCysGlyMetLeuHisLysHisGlnLeuGlyLysValTyrArgAsp 316
Db      877 GCTGCAAGCTGTGTGGCTTGGCTTGGAGATTTACAGAGGAGAAAGATTTGTATACAGAGAC 936
Qy      317 MetLysProGlnLysAsnValLeuLeuAspAspLeuGlyLysCysArgLeuSerAspLeuGly 336
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Qy      337 LeuAlaValGlnMetLysGlyLysProIleThrGlnArgLysAlaThrAsnGlyTyr 356
Db      997 TTGGCCACAGAGATCCAGAAAGACAGAGGTTGAGAGAAAGTTGAAACAGTGGCTAC 1056
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Db      1057 ATGGCACTTGAAGTTGTCAATATATGA---AAGTATACGTTTATGTCGATTTGGTGGGA 1113
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Qy      437 GlnArgLeuLysSerArg---GlnLysSerAspAspProArgLysHisPhePheLys 455
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Db 464 AA

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Db      1583  GTGAGGCGCTCAATCTGGACACACAGACGACTTCTACTCCAAGTTCTCCAGCGGC 1642
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Db      1643  TCTGTGTCCATCCATGCGCAAAACGAGATGATGAAACAGATGCTTTAAGAGACTGAAC 1702
Qy      532  -----AspPro-AspAr 535
Db      1703  GTGTTGGACCTAATGATGACCTCCCGCCAGATCTGAACGAAACCACTTCGGAACCG 1762
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Search completed: August 13, 2004, 21:21:52
 Job time : 573 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 17:28:46 ; Search time 4223 Seconds
(without alignments)
5675.751 Million cell updates/sec

Title: US-10-044-205A-2
Perfect score: 2889
Sequence: 1 WVDGALDNLNLTANTAYLQAR.....NRPCTGEEGNSKSGVCLLL 553

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=genfmd1 -OPMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
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-OUTPMT=PIO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044205 @CNC 1.1 2568 @runat 06082004.104322.23357 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb hcg:*
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11: gb sts:*
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26: em sts:*
27: em un:*
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29: em vi:*
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35: em hcg_rtd:*
36: em hcg_mam:*
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41: em hcg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2889	100.0	2198	6 AX797552	AX797552 Sequence
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4	2883	99.8	1662	6 AX252439	AX252439 Sequence
5	2883	99.8	1662	6 AX642968	AX642968 Sequence
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7	2883	99.8	1799	9 AR439409	AR439409 Homo sapi
8	2883	99.8	2249	6 AR225819	AR225819 Sequence
9	2883	99.8	2249	6 AX252443	AX252443 Sequence
10	2883	99.8	3186	6 AX710216	AX710216 Sequence
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12	2876	99.6	1662	6 AR263766	AR263766 Sequence
13	2876	99.6	1662	6 AR343544	AR343544 Sequence
14	2876	99.6	1662	6 AX357902	AX357902 Sequence
15	2868	99.3	1662	6 AX166511	AX166511 Sequence
16	2868	99.3	1662	6 AX710213	AX710213 Sequence
17	2823.5	97.7	1701	6 AX921933	AX921933 Sequence
18	2507.5	86.8	2420	4 AY049726	AY049726 Bos tauru
19	2502	86.6	2453	4 AF282270	AF282270 Sus scrof
20	2459	85.1	3095	10 AF063016	AF063016 Spermophi
21	2058	71.2	1191	6 BD186106	BD186106 A novel g
22	1801	62.3	1062	6 AR225818	AR225818 Sequence
23	1801	62.3	1062	6 AX252441	AX252441 Sequence
24	1700	58.8	2954	5 AB009568	AB009568 Oryzias 1
25	1665	57.6	2898	5 AB055658	AB055658 Cyprinus
26	1528	52.9	36651	6 AR263767	AR263767 Sequence
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36	1268.5	43.9	1952	9 HSU63973	U63973 Human rhodo
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45	1252.5	43.4	2511	6 AX427344	AX427344 Sequence

ALIGNMENTS

RESULT 1

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LOCUS AX797554 1659 bp DNA linear PAT 04-OCT-2003
DEFINITION Sequence 3 from Patent WO02095032.
ACCESSION AX797554
VERSION AX797554.1 GI:37518056
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kapeller-Liebermann, R. and Bandaru, R.
METHOD and compositions of human proteins and uses thereof
Patent: WO 02095032-A 3 28-NOV-2002;
MILENITUM PHARMACEUTICALS, INC. (US)
FEATURES
source location/qualifiers
1..1659
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7,03e-251 Length: 1659
Score: 2889.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgSerLeuAlaLeuPro 40
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DB 121 GGGCTGGAGGGCTGGCGGAGCTCCGCCAAGAGCTGCTCCGAACTTCCACAGCTGTGT 180
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DB 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTTGTGCTAAAGAACAGAGCAAGGCTTAGGA 1320
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DB 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAACATATTTCTTAAACGATCACTTCTCT 1380
QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGlnPheAspAspLys 500
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QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
DB 1501 GATPAGAGTCTTCAAAAACCTTGGGACAGGTGCTGTCTTATACATGGCAAGAAAGAA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
DB 1561 ATTATGAAAACGGGACTGTTTGGAGAACTGAATGACCCCAACAGACTTACGGGTGTGAG 1620
QY 541 GluGlyLysAsnSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGATTAATTCATCCAGTCTGGCGTGTGTGTATTTG 1659
RESULT 2
AX797552

LOCUS AX797552 2198 bp DNA linear PAT 04-OCT-2003
 DEFINITION Sequence 1 from Patent WO02095032.
 ACCESSION AX797552
 VERSION AX797552.1 GI:37518055
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Kapeller-Libermann, R. and Bandaru, R.
 AUTHORS
 TITLE Method and compositions of human proteins and uses thereof
 JOURNAL Patent: WO 02095032-A 1 28-NOV-2002;
 MILENITUM PHARMACEUTICALS, INC. (US)

FEATURES
 Source Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1.01e-250 Length: 2198
 Score: 2889.00 Matches: 553
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-044-205a-2 (1-553) x AX797552 (1-2198)

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 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 471 GAGCAACAGCCCATGGATCGCGCTCTTCCGTGACTTCTGACCAAGTCCCACTTC 530
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyPro 100
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 QY 201 GlyPheGlyGlnValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220

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 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGln 340
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RESULT 3
 LOCUS AR225817 1662 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 1 from patent US 6444456.
 accession AR225817
 version AR225817.1 GI:27263947
 keywords
 source Unknown.
 organism Unknown.
 reference 1 (bases 1 to 1662)
 authors Walke, D.W., Milgowski, N.L. and Turner, C.A. Jr.
 title Human G-coupled protein receptor kinases and polynucleotides encoding the same
 journal Patent: US 6444456-A 1 03-SEP-2002;
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ORIGIN

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Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	6	Gaps:	0

US-10-044-205A-2 (1-553) x AR225817 (1-1662)

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DB      61 AACCTCTGCGACTGCGACACCAAGAGCTGCGAGCGGGCGGCGCTGAGCTGGCCCTGCC 120
QY      41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAspPheHisSerLeuCys 60
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QY      61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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QY      321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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 DEFINITION Sequence 1 from Patent WO0168869.
 accession AX252439
 AX252439.1 GI:15985733

KEYWORDS

Homo sapiens (human)
SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Walke, D.W., Wilganowski, N.L. and Turner, C.A.
Human g-coupled protein receptor kinases and polynucleotides
encoding the same

TITLE

Patent: WO 0168869-A 1 20-SEP-2001;
Lexicon Genetics Incorporated (US)

JOURNAL

FEATURES

source

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ORIGIN

Alignment Scores:

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Score:	2683.00	Matches:	552
Percent Similarity:	99.82%	Conservative:	0
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	99.79%	Indels:	0
DB:	6	Gaps:	0

US-10-044-205a-2 (1-553) x AX252439 (1-1662)

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LOCUS AX642968
DEFINITION Sequence 45 from Patent WO01096547.
ACCESSION AX642968
VERSION AX642968.1 GI:28550117

KEYWORDS
SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

Yue, H., Lai, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y., Gandhi, A.R., Tribouley, C.M., Wallis, N., Yao, M.G., Lu, D.A., Greenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N., Nguyen, D.B., Tang, Y.T., Baughn, M.R., He, A., Thornton, M., Hatalla, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F., Reicion, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M., Elliott, V.S., Thangavelu, K., Batra, S. and Ison, C.H.

TITLE
JOURNAL
Human Kinases
Patent: WO 01096547-A 45 20-DEC-2001;
Incyte Genomics, Inc. (US)

FEATURES
source

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ORIGIN

Alignment Scores:

Pred. No.: 2,456-250 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

US-10-044-205A-2 (1-553) x AX642968 (1-1662)

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REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 1799) Chen,C.-K., Zhang,K., Church-Kopish,U., Huang,W., Zhang,H., Chen,Y.J., Frederick,J.M. and Baehr,W.
TITLE	Characterization of human GRK7 as a potential cone opsin kinase
JOURNAL	Mol. Vis. 7, 305-313 (2001)
MEDLINE	21626361
PMID	11754336
REFERENCE	2 (bases 1 to 1799)
AUTHORS	Baehr,W. and Chen,C.-K.
TITLE	Direct Submission
JOURNAL	Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15 North/2030 East, Salt Lake City, UT 84112, USA
FEATURES	Location/Qualifiers
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 KEYWORDS
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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2249)
 AUTHORS Malke, D.W., Wilganowski, N.L. and Turner, C.A. Jr.
 TITLE Human G-coupled protein receptor kinases and polynucleotides
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 1 Malke, D.W., Wilganowski, N.L. and Turner, C.A.
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AUTHORS
 TITLE
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 Patent: WO 0168869-A 5 20-SEP-2001;
 Human g-coupled protein receptor kinases and polynucleotides
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ORIGIN

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 Query Match: 99.79% Indels: 0
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 CHORDATA; Chordata; Craniota; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1
 AUTHORS Xia, Y.
 TITLES Regulation of human g protein-couple receptor kinase
 JOURNAL Patent: WO 03018615-A 4 06-MAR-2003;
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS Weis, E.R., Ducceschi, M.H., Horner, T.J., Li, A., Craft, C.M. and Osawa, S.
 TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction
 JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)
 MEDLINE 11717351
 PUBMED 21574315
 REFERENCE
 AUTHORS Osawa, S. and Weis, E.R.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA

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 Best Local Similarity: 99.82% Mismatches: 1
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Guegler, K., di Francesco, V. and Beasley, E. M.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding
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 JOURNAL Patent: WO 0192496-A 1 06-DEC-2001;

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 Plozman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
 Flanagan, P. and Clardy, D.S.
 TITLE Novel human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0138503-A 2 31-MAY-2001;

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 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGAGCGCTGACGGGGCTGGTGCACCTTGTCAGTGTCCCTGCGCCGCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAAAGCGAGTGGCTGACGTGACGCTGGCCAAAGCTGAGGCAATGCTTCTTGCAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTropLysLeu 180
 Db 481 CACCCCTTTAAGATTTCTGACACGAGCGCTTCTCAAGAAATTTCTGAGTGGAGAACTC 540
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 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGATGATGTCCTCCAGGTGAAAACACTGGGAGAGATGCTGTAAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
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 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetLeuGlyLysAspLeuLysPheHisIle 280
 Db 781 AAGACCATCTCTGCTTGTCTATGAGCTCTGATGAAATGGGGGAGACCTCAAGTTCACATC 840

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QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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QY 421 GlnGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
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QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
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QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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DB 1621 GAGGGTAAATTCATCCAAAGCTGGGGTGTGTTGTTATTG 1659
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Job time : 4257 secs

Bulk Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 16:49:07 ; Search time 449 Seconds

(without alignments)
5232.191 Million cell updates/sec

Title: US-10-044-205a-2
Perfect score: 2889

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Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	2876	99.6	1662	6 AAD28071
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12	2868	99.3	1662	7 ACC44826
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15	1801	62.3	1062	4 AAh78798
16	1528	52.9	36651	6 AAD28072
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18	1252.5	43.4	2511	2 AAV71032
19	1252.5	43.4	2519	7 ACA03892
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38	1189	41.2	1983	2 AAO87427
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42	852.5	25.5	1316	7 ABB74511
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ALIGNMENTS

RESULT 1
ID ABS57375
XX ABS57375 standard; cDNA; 2198 BP.
XX AC ABS57375;
XX DT 04-FEB-2003 (first entry)
XX DE cDNA encoding human GPCR kinase (GPCRK) 69087.
XX KW Human; G protein coupled receptor kinase; GPCR 69087;
XX KW cellular proliferative disorder; differentiative disorder;
XX KW haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
XX KW metastatic disorder; cytostatic; gene therapy; gene; ss.
XX OS Homo sapiens.

Key Location/Qualifiers
FT CDS 291..1952
FT /tag= a "GPCRK 69087"
FT /product= "GPCRK 69087"
FT /note= "The coding sequence given as SEQ ID No:3 is specifically claimed in Claim 1"

US2002123464-A1.
05-SEP-2002.
22-OCT-2001; 2001US-00044205.
19-OCT-2000; 2000US-0241884P.
20-OCT-2000; 2000US-0241877P.

PR 23-OCT-2000; 2000US-0242428P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Kappeler-Libermann R, Bandaru R;
 PI
 XX WPI; 2003-066811/06.
 DR P-PSDB; AB672173.
 XX
 PT Novel isolated G protein coupled receptor kinase, 69087, nuclear
 PT signaling protein, 15821 or mitogen activated protein kinase phosphatase,
 PT 15418, useful for treating cellular proliferative or differentiative
 PT disorders.

PS Claim 1; Fig 1; 989P; English.

XX The present invention relates to the isolation of a novel human G protein
 CC coupled receptor (GPCR) kinase (GPCR) designated 69087, a novel human
 CC nuclear signalling protein designated 15821, and a novel human mitogen-
 CC activated protein kinase (MAPK) phosphatase MAPK designated 15418, and
 CC the polynucleotide sequences encoding them. The sequences of the
 CC invention are useful for treating and diagnosing disorders such as
 CC cellular proliferative and differentiative disorders (e.g. haematopoietic
 CC neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
 CC disorders). They are also useful in screening assays, detection assays
 CC (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
 CC trials and pharmacogenomics), and in methods of treatment (e.g.
 CC therapeutic and prophylactic). The sequences may also be used to screen
 CC public databases to identify other family members or related sequences.
 CC The polypeptide sequences are useful as immunogens to generate antibodies
 CC that bind the polypeptides. The polynucleotide sequences are useful for
 CC mapping their respective genes on a chromosome, identifying gene regions
 CC associated with cellular proliferative or differentiative disorders, and
 CC in gene therapy. The present sequence encodes human GPCR 69087

XX Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.78e-282 Length: 2198
 Score: 2889.00 Matches: 553
 Percent Similarity: 100.00% Conservative: 0
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US-10-044-205A-2 (1-553) x ABS57375 (1-2198)

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 QY 161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
 Db 771 CAGCCCTTTAAGGATTCGTGACCAACCGCTTCTTACCAACAGATTTCTGCAATGGAACTC 830
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 QY 241 GlnLeuLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 1011 GAATCTTGAGAGAGTGCAGAGCCCTTTCATGTTCTCTGCGCTATGCTTGAAGGC 1070
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
 Db 1071 AAGACCATCTCGCTGCTGTGATGAGCTGATTAAGAGGAGACCTTCAAGTTCCACATC 1130
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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 Db 1251 AATGCTCTTCTGAGTGAAGCTCGGCAACTGCAAGTTATCTGACCTGGGCTGGCGTGAG 1310
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for generating antibodies, as reagents in diagnostic assays for

281 TyrAsnValGlyThrArgGlyLeuAspMetSerAroValTlaphaThrCovAl-CT-11

Db 841 TACACGCTGGGACCGGCTGGAGACGAGCGGAGTCTTTTACCTGGCCCAAGTA 900
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 DT
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 DE Novel human gene. SEQ ID 49.
 XX
 XX Human: cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
 KM neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KM antiinflammatory; cardiant; antidiabetic; antitumor; antihypertensive;
 KM cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
 KM wound healing disorders; atherosclerosis; Parkinson's disease;
 KM Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KM inflammation; neoplastic disease; nervous system disorder;
 KM cardiovascular disorders; pancreatitis; respiratory disorder;

KM hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KM developmental abnormality; gastrointestinal ulceration; neuropathy;
 KM haematological disease; metabolic disease; brain damage; colitis;
 KM thyroid disorder; hypothyroidism; neurological disease; stroke;
 KM cone photo- transduction deficiency; neurological disease; heart;
 KM angiodysplasia; ovulation disorder; spinal cord; thyroid gland; heart;
 KM trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KM growth abnormality; precocious puberty; gene; ss.
 OS Homo sapiens.
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 PN W0200250105-A1.
 PD 27-JUN-2002.
 XX
 PF 17-DEC-2001; 2001WO-US049232.
 XX
 XX 19-DEC-2000; 2000US-0256710P.
 PR 20-DEC-2000; 2000US-0257048P.
 PR 09-JAN-2001; 2001US-0260482P.
 PR 30-JAN-2001; 2001US-0264922P.
 PR 06-FEB-2001; 2001US-0266797P.
 PR 19-MAR-2001; 2001US-0276988P.
 PR 04-APR-2001; 2001US-0281535P.
 PR 08-MAY-2001; 2001US-0283622P.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 PA Agarwal P, Birkeland M, Cogswell JP, Kahnack KF, Lai Y,
 PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
 PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
 DR WPI: 2002-508784/54.
 DR P-PSDB; ABP61013.
 XX
 XX Secreted proteins and polynucleotides useful as vaccines for preventing
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
 PS Claim 2(a); Page 255-256; 335p; English.
 XX
 XX The invention relates to an isolated polypeptide with signal sequences
 CC which allow it to be secreted extracellularly or membrane associated. The
 CC activity of polypeptides of the invention may be described as,
 CC cyostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, neurotropic,
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, anorectic,
 CC cardiant, antidiabetic, antitumor, antihypertensive, cancer, infection;
 CC and metabolic. Polypeptides and polynucleotides of the invention are
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,
 CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
 CC inflammation, neoplastic diseases, nervous system related disorders and
 CC cardiovascular disorders, pancreatitis, respiratory disorder,
 CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,
 CC haematological diseases, metabolic diseases, brain damage, colitis, cone photo-
 CC disorders e.g. hypothyroidism, neurological diseases, stroke, angiodysplasia,
 CC transduction deficiency, neurological diseases, heart, thyroid gland, heart,
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
 CC growth abnormalities, and alleviation of precocious puberty. The
 CC sequences given in records AB086130-AB086184 represent novel human cDNA's
 CC of the invention
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 SO Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

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 Best Local Similarity: 99.82%
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 Conservative: 1
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DB: 6 Gaps: 0

US-10-044-205a-2 (1-553) x AB086178 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspSerLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20

DB 1 ATGTGACATGGGGGCGCTGACCAACTGATGCGCAACACCGCTACCTGGAGCGCG 60

QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGACCTGCGACAGCAAAAGCTGGAGCGCGCGCTGACCTGGAGCGCGCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGluLysLeuSerLeuAsnProHisSerLeuCys 60

DB 121 GGGCTGCGAGGGCTGGCGGAGCTCGCCCAAGACTCTCCCTGAACCTTCACAGCGCTGCT 180

QY 61 GluGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe 80

DB 181 GAGCAGACGCCCATCGGTGCGCGCTCTTCCTGACTTCCTAGCCACAGTGGCCACGTTT 240

QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnProGluLeuAlaGluGlnGlyPro 100

DB 241 CGCAGGCGCGCAACCTTCTTGAGAGAGCTGCAAACTGGAGCTGGCGCAGAGGAGACC 300

QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

DB 301 ACCAAGACAGCGCGCTGCGAGGGCTGAGGCACTTGCGAGTTCCTGCGCGCGCG 360

QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140

DB 361 AACCCCAACCTTCTCTGACCGAGCGCGCTGCGACCAAGCGCAAGCGCAACCGACCTGAG 420

QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160

DB 421 GAAGAGCGAGTGGCTGCGAGCGCTGGCGCAAGCTGAGCGCATGGCTTCTTGGCAAG 480

QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnProLysLeu 180

DB 481 CGGCCCTTAAAGATTCGTGACCAAGCGCTTCAAGCAAGTTTCTGCGAGTGAACCTC 540

QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200

DB 541 TTGAGATGCAACAGGTGACAGCAAGACTTCACTGAGTTCAGAGTCTGGGAAAGCT 600

QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220

DB 601 GGTTTTGGAGAGTATGCTCTCGAGTGAAGAAACAGTGGAGAGATGATCGCTGTAG 660

QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGlnLys 240

DB 661 AAACGTGACAAAGAGCGCTGACAAAGAAAGTGGCGAAGATGGCTCTTGGAAAG 720

QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260

DB 721 GAATCTTGGAGAAAGGTGACAGCGCTTCACTGCTCTGCGCTATGCTCTTGAAGC 780

QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyLysPheLysPheHisIle 280

DB 781 AAGACCATCTGCTGCTGATGACGCTGATGAATGGGGAGAACCTCAAGTTCACATC 840

QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300

DB 841 TCAACGTGGACACCGCTGCTGACATGAGCCGGGTGATCTTTTACCGCCCGAGAA 900

QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320

DB 901 GCTGTGGATGCTGACCTTCATGAACTCGGCACTCTATCGGAGCATGAGCCGTGAG 960

QY 321 AsnValLeuLeuAspAspLeuGlyLysCysArgLeuSerAspLeuGlyLysAlaValGlu 340

DB 961 AATGTCTTCTGATGACCTCGGCAACTGCGAGTTTATCTGACCTGGGCGCTGGAG 1020

QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360

DB 1021 ATGAGAGGTGCGACAGCCCATACCCAGAGCGCTGGACCAATGTTACATGCTCTCTGAG 1080

QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspThrPheAlaMetGlyCysSer 380

DB 1081 ATCTTAATGAAAGAGTAAAGTAAATTTCTATCTCTGAGACGTGTTTCCATGGAGATGACGC 1140

QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

DB 1141 ATTATGAATGATGTGTCGACGACCAACCATTTCAAAATTTACAGAGAAAGTCAATAA 1200

QY 401 GluAspLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAAAGATTTGCGAGGCTCTTCTGCTAGAGAAACAGCAACGCTTAGA 1260

QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440

DB 1261 GAGCAAGCAAAAGATTTGCGAGGCTCTTCTGCTAGAGAAACAGCAACGCTTAGA 1320

QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnProPro 460

DB 1321 AGCAGAGAAAGTCTGATGATCCAGAAACATCATTTCTTTAAAGATCAACTTTTCTC 1380

QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValTyrAla 480

DB 1381 CGCTCGAGAGCTGCTTAATTTGAACCCCATTTGTGCGAGACCTTCAGTGGTTTATGCC 1440

QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500

DB 1441 AAAGCAATCGCTGAATTTATGATATTTCTGAGAGTTCGGGGGGTGGAAATTTATGACAAA 1500

QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaProGlnGlu 520

DB 1501 GATTAAGCATTTCTTCAAAAACCTTGGCAAGGCTGCTTCTTACACAGCGAGAGAA 1560

QY 521 IleIleGlnThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540

DB 1561 ATTATGAAGCGAGCTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGTAG 1620

QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553

DB 1621 GAGGATATTTATCCAGACTGCGCGGTGTGTATG 1659

DB 1659

RESULT 4

ID AAD26466 standard; cDNA; 1662 BP.

AC AAD26466;

XX XX

DT 26-MAR-2002 (first entry)

XX XX

DE Human kinase PKIN-19 cDNA.

XX XX

XX Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; diabetes mellitus; osteoarthritis; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy; ss.

OS Homo sapiens.

XX XX

XX Key

XX CDS

FT 1..1662

FT /tag= a

FT /product= "Human PKIN-19 protein"

PN MO200196547-A2.

XX 20-DEC-2001.
 PD 14-JUN-2001; 2001WO-US019444.
 XX 15-JUN-2000; 2000US-021073P.
 XX 23-JUN-2000; 2000US-0213467P.
 PR 30-JUN-2000; 2000US-0215651P.
 PR 07-JUL-2000; 2000US-021605P.
 PR 13-JUL-2000; 2000US-0218372P.
 PR 25-AUG-2000; 2000US-0228056P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y,
 PI Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
 XX WPI: 2002-090207/12.
 DR P-PSDB; AAE16273.
 XX New polypeptides, useful for diagnosing, treating or preventing disorders
 PT of growth and development, cardiovascular and lipid, and diseases such as
 PT cancer, comprise human kinase polypeptides.
 XX
 XX Claim 5; Page 190; 197pp; English.
 XX The invention relates to human kinase PKIN proteins and their
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for
 CC treating a disease or condition associated with decreased expression of
 CC PKIN and a composition comprising PKIN antagonist is useful for treating
 CC a disease or condition associated with overexpression of PKIN. The
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 CC mellitus, multiple sclerosis, gout, psoriasis, Crohn's disease, diabetes
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Retter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cirrhosis, hepatitis,
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 CC hypocholosterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 CC of a test compound and in gene therapy. The present sequence is human
 CC PKIN-19 cDNA
 XX
 XX Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 SQ
 XX Alignment Scores: Length: 1662
 XX Pred. No.: 2885.00 Matches: 552
 XX Score: 2885.00 Conservative: 0
 XX Percent Similarity: 99.82% Mismatches: 1
 XX Best Local Similarity: 99.82% Indels: 0
 XX Query Match: 99.79% Gaps: 0
 DB: 6
 US-10-044-205a-2 (1-553) x AAD26466 (1-1662)
 QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGGTGAACATGGGGCCCTGGACCACTGATCCCAACGCCCTACCTCCAGGCCCG 60
 QY 21 LysProSerAspCysAspSerIleGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCCTCGGACCTGGACAGCAAGAGAGCTGGACGCGCGGCGCTAGCTGCGCCCTCC 120

QY 41 GlyLeuGlnIleCysAlaGlnLeuArgGlnIleLysLeuSerLeuAsnPheHisSerLeuCys 60
 DB 121 GGGCTGACAGGGCTGCGCGAGAGCTCGCCAGAGAGCTGCTCCGAACTTCCACAGCTGTGT 180
 QY 61 GluGlnGlnIleProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCCATCGATCGCGCTCTTCCGTGATCTTCCAGCCAGCGCCACAGCTTC 240
 QY 81 ArgGlySalAlaThrPheLeuGlnAspValGlnAsnTyrGlnLeuAlaGluGluGlyPro 100
 DB 241 CGAAGCGCGCAACTTCTCTAGAGAGCTGCAAGCTGGAGACTGGCGCGAGGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnIleLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAGACAGCGCGCTGCGAGGGCTGGTGGCACTTGCGAGTGGCCCTGCGCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCCGAACTTCTCTACCGACGCGCGCTGGCCCAAGGCGCAAGCCACAGCCACTGAG 420
 QY 141 GluGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGly 160
 DB 421 GAAAGCGAGTGGCTGCGAGTACGCTGCGCAAGGCTGAGGCTGAGCTTTCTTGCAAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 DB 481 CAGCCCTTGAAGATTTGTGACCGAGCGCTTTCACAGAACTTTCGACAGTGAATCTC 540
 QY 181 PheGlnLeuGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 DB 541 TTCGAGATGACACAGCTGACAGAGTACTCAGTGTCTGAGGCTGCGGAAAGT 600
 QY 201 GlyPheGlyGlnValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 DB 601 GCTTTTGGGAGGTATGCTCGCTCAGGTGAAAACACTGGGAAAGATGATGCTGCTGAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlnLysMetAlaLeuLeuGlyLys 240
 DB 661 AAATCGACAGAGAGCGGTGAAAGAAAGGTGGCGAGAAAGATGGCTCTTGAGAAAG 720
 QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 DB 721 GAAATCTGGAAAGTCAAGAGCCCTTATGCTCTCTGCGCTATGCTTTGAGAAC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 DB 781 AAGACCATCTCTGCTGCTGATGAGCTGATGAAATGGGAGAGCTTCAAGTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 841 TACAACTGGGACGCGGTGGCTGACATGAGCCGGGTATCTTTTACTCGGCCCAAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 DB 901 GCGTGGAGATCTGCACTTCATGAACTCGGACATCGCTATGCGGACATGAACCTTGA 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 DB 961 AATGTGCTTCTGATGACCTCGGACCTGAGTATATCTAATCTGCGGCTGGCGCTGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 DB 1021 ATGAAGAGGTGGCAAGCCATTAACCAAGAGGCGTGAACCAATGATTAACAGTCTCGAG 1080
 QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGAAAGAGTAAGTATATCTAATCTGAGCTGTTGCACTGGGAGAGCAGC 1140
 QY 381 IleTyrGlnLeuValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400
 DB 1141 ATTATGAAATGCTGCTGAGCAACACATTCAAAGATTACAGAGAAAGAGTCAAGTAAA 1200

QY 401 GluAspLeuYSGlnArgThrLeuGlnAspGluValIleuYleuPheGlnHisAspAspPheThr 420
 Db 1201 GAGCATCTGAGCAAGAACTCTGCAAGACAGAGTCAATTCAGCATGATACCTTCA 1260
 QY 421 GluGluAlaIleAspIleCysArgPheLeuAlaIleuPheGlnArgLeuGly 440
 Db 1261 GAGGAGCAAAAGATTTTGCAGGCTCTTCTGCTTAAGAACAGAGCAACCTTACGA 1320
 QY 441 SerATGGIuYSerSerAspAspProArgIleHisIlePhePheThrIleAspPhePro 460
 Db 1321 ACCAGAGAAAAGTCTGATGATCCAGAAACATCATTTCTTTAAACGATCAACTTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValIleVal 480
 Db 1381 GCGCTGGAAGCTGCTTATTTGAACCCCATTTGTCAGACCCCTTCATGTTTATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValIlePheAspAsp 500
 Db 1441 AAAGACATCGCTGAATTTGATGATTTCTCTGAGGTTGCGGAGGATGGAATTTGATGACAA 1500
 QY 501 AspLysGluPhePheLysAspPheAlaThrGlyAlaValProIleIleThrGlnGlu 520
 Db 1501 GATAGCATGTTCTCAAAAACCTTGGACAGGCTCTTCTTATGACATGGCAGGAAGA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAspProAspArgProThrGlyCysGlu 540
 Db 1561 ATTATGAAAGCGAGCTGTTTGAAGACTGATGACCCCAACAGACTACGGGTTGTGAG 1620
 QY 541 GluGlyAsnSerSerIleYSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGGTAATTCATCCAGCTCGCTGTGTTGTATTTG 1659

RESULT 5
 AAD46350
 ID AAD46350 standard; cDNA; 1662 BP.
 AC AAD46350;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Human cone opsin kinase (GRK7) cDNA.
 XX
 KW Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW chronobiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "Human GRK7 protein"
 XX
 PN W0200272541-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 07-MAR-2002; 2002W0-US007025.
 XX
 PR 07-MAR-2001; 2001US-0274006P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Bird TA, Spencer M, Mosley BA;
 XX
 DR WPI; 2002-723307/78.
 DR P-PDB; AAE28952.
 XX
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual

PT signaling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4, Page 45-46; 61pp; English.
 CC
 CC The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signalling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC blindness), pineal gland activity (e.g., chronobiological desynchrony,
 CC or jet lag), agonists of GRK7 polypeptide activity may be used to treat
 CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC preparation of a medication for treating a condition or disease related
 CC to cone photoreceptor visual signalling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for
 CC individuals with such disorders. The present sequence is human GRK7 cDNA
 XX

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.:
 Score: 7,616-282
 Percent Similarity: 2883.00
 Best Local Similarity: 99.82%
 Query Match: 99.82%
 DB: 99.79%
 Gaps: 0

US-10-044-205A-2 (1-553) x AAD46350 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaIleuGlnAlaArg 20
 Db 1 ATGTGTGACATGAGGGGCTCTGAGCAACCTGATGCGCAACCGCTTACCTGACGGCCGG 60
 QY 21 LysProSerAspCysAspSerIleuGlnArgAlaGlyGlySerLeuAlaLeuPro 40
 Db 61 AAGCCTTCGAGTGGACAGCAAGAAAGCTGACGCGCGCGCTGAGCCCTGCGCC 120
 QY 41 GlyLeuGlnIleCysAlaGluLeuArgGlnIleuSerLeuAspPheHisSerLeuCys 60
 Db 121 GGGCTGAGGAGGCTGCGCGAGCTCCGCAAGAGCTGCTCCGAACTTCCACAGCCCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGAGAGCCATGCTGCTGCGCTCTTCCGTGACTTCTTACGCAAGTCCACGCTTC 240
 QY 81 ArgIleAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlnIlePro 100
 Db 241 CGCAAGCGCGCAACCTTCTTACGAGCACTGCAAGATCGGAGCTGCGAGAGAGGACCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGAGAGAGGCGCTGCGAGGCTGCTGCGCACTTGTGCAAGTCCCTGCGCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCGCAACCTTCTTCCAGCAAGCGCTGCGCAACCAAGTCCCAAGAGCGCAACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgIleAlaGluAlaMetAlaPheLeuGlnIle 160
 Db 421 GAAAGAGCAGAGGCTGCTGAGTGAAGCTGAGGCAAGGCTGAGGCTTCTTTCGCAAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyraAspLysPheLeuGlnTrpLysLeu 180


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481 CAGCCCTTAAAGATTTCGTGACGAGGCTTCTACGACAAAGTTTCGACGAGGAAATC 340
181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
541 TTGAGATGACAAACGATGACGACAAAGTACTGACGATTCAGAGGTGCGGAAAGGT 600
201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetCysAlaCys 220
601 GGTGTTGGGAGATGATGCTGCTGAGGTAAGAAACCTGGAGAGATGATGCTGTAAG 660
221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGlyLys 240
661 AAACGTGACAAAGAGCGCTGAAGAGAAAGTGGCGAGAAAGTGGCTCTTGGAAAG 720
241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
721 GAAATCTGAGAAAGTCAAGAGCCCTTCAATGCTCTCTGCTGCTGCTGCTGAGAGC 780
261 LysThrIleLeuCysLeuValMetSerLeuMetLanGlyValAspLeuLysPheIle 280
781 AAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerIleGlnIle 300
841 TACAACGTGGGCAACGGTGGCTGACATGACCGGGGATCTTTTACTGCTGCTGCTGCT 900
301 AlaCysGlyMetLeuIleLeuIleGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
901 GCTGTGGAGTCTGACCTCCATGAACTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCT 960
321 AsnValLeuLeuAspAspLeuGlyLysAsnCysArgLysSerAspLeuGlyLeuAlaGlu 340
961 AATGGCTTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
341 MetLysGlyGlyLysProIleThrGlnArgIleGlyThrAsnGlyTyrMetAlaProGlu 360
1021 ATGAAAGGTGGCAAGCCCATCATCCAGAGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
361 IleLeuMetGluLysValSerTyrSerTyrProValAspThrPheAlaMetGlyCysSer 380
1081 ATCTTAATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1140
381 IleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
1141 ATTATGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnIleAspAsnPheThr 420
1201 GAGGATCTGAAAGCAAAAGTCTGCAAGAGAGAGTCAAAATTCAGCATGATTAATCTTACA 1260
421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
1261 GAGGAAACAAATAATTTGAGGCTCTCTTGGCTAAAGAACCAAGACGCTTGAAGA 1320
441 SerArgGlnLysSerAspAspProArgLysIleSphPheLysThrIleAsnPhePro 460
1321 AGCAGAGAAAGTCTGATGATCCAGAAACATCACTTTCTTAAAGATCAACTTCTTCT 1380
461 ArgLeuGluIleGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
1381 CCGCTGGAAGCTGCTGCTTAATGAAACCCCATTTGCTCCAGACCTTCAAGGTGTTATGCC 1440
481 LysAspIleAlaGluIleAspAspPheSerGluValArgIleValGluPheAspAspLys 500
1441 AAGAGCATGCTGAAATTTGATGATTTCTGAGGTTCGGGGGTGGAATTTGATGACAA 1500
501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGluGlu 520
1501 GATTAAGCATTTCTTCAAACTTTGAGACAGGTCTGCTTCAATGATGCTGCGAGAGAA 1560
521 IleIleGluThrGlyLeuPheGluGluLeuLeuAsnProAsnArgProThrGlyCysGlu 540

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DB 1561 ATTATGAAACGAGCTGTTGAGGACTGAATGACCCCAAGACCTAGGGTTGTAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
DB 1621 GAGGTAATTCATCAAGTCTGCGGTGTTGTTATTTG 1659
RESULT 6
ABZ56943
ID ABZ56943 standard; DNA; 1761 BP.
AC
ABZ56943;
XX
XX 04-APR-2003 (first entry)
DT
DE Human gene sequence relative to the invention # SEQ ID 11.
XX
XX Human: heart disease; cancer; omentopathy; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 26..1687
XX FT /*tag= a
XX
XX WO2002103020-A1.
XX
XX 27-DEC-2002.
XX
XX 14-JUN-2002; 2002WO-JP005942.
XX
XX 15-JUN-2001; 2001JP-0018254.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Koyama N, Tanida S, Yamamoto K;
XX
XX WEI; 2003-157045/15.
XX
XX P-PSDB; ABP6079.
XX
XX Novel disease-associated gene of the RGS gene family and its product,
XX applicable in diagnosis of and screening for drugs for heart diseases,
XX cancers and omentopathy.
XX
XX Example 3, Page 85-86; 96pp; Japanese.
XX
XX The invention relates to a novel disease associated gene and its uses.
XX The gene and its encoded protein are useful for diagnosis of and
XX screening for drugs for heart diseases, cancers and omentopathy. The
XX current sequence represents a human gene sequence relative to the
XX invention
XX
XX Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
SQ
Alignment Scores: 1761
Pred. No.: 8,25e-282
Score: 2883.00
Percent Similarity: 99.82%
Best Local Similarity: 99.82%
Query Match: 99.79%
DB: 7
US-10-044-205A-2 (1-553) x ABZ56943 (1-1761)
QY 1 MetValAspMetGlyValAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
DB 26 ATGCTGAGACATGCGGGGCTCTGAGAACCTGATCGCAACACCCCTACCTGACAGCCCG 85
QY 21 LysProSerLysCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 86 AAGCCTCGAGCTGCGACAGCAAGAGCTGACAGCGCGCGGTAGCTGCGCTGCCCC 145
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheIleSerLeuCys 60

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QY	421	GLUGluAlaIyAsp11eCysArgLeuAlaIyAspProGluGlnArgLeuGly	440
Db	1286	GAGAGGCAAAAGATATTGGAGGCTCTTTCGCTTAAGAAACCAAGACGCTTAGA	1345
QY	441	SerArgIuIySerSerAspProArgIySerHisphelSerThrIleAsnPro	460
Db	1346	AGCAGAGAAAGCTGATGATCCAGGAAACATCATTTCTTTAAACATCACTTCCCT	1405
QY	461	ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValIlyVala	480
Db	1406	CGCGTGAAGCTGGCTTATTTGAACCCCATTTGGCGAGACCTTACAGGTTTAGCC	1465
QY	481	IyAsp11eAlaGluIleAspAspPheSerGluValArgIyValGluPheAspIyS	500
Db	1466	AAAGACATCCCTGAATTGATGATTTCTCTAGAGTTTGAGGAGGAGAAATTGATCAAA	1525
QY	501	AspIyGlnPhePheIyAsnPheAlaThrIyValaValProIleAlaTyrGlnGluGlu	520
Db	1526	GATTAACGATGTTCTCAAAAACITTTGGACAGAGTGCCTGCTTTCATGACATGAGGAGAA	1585
QY	521	IleIleGlnThrGlyLeuPheGlnGluLeuAsnAspProAsnArgProThrIyCysGlu	540
Db	1586	ATTATAGAAACCGGACCTTTTGAGAACTGAATGACCCCAACAGACCTACGAGTTTGAG	1645
QY	541	GluGluAsnSerIySerGlyValCysLeuLeu	553
Db	1646	GAGGGTAAATTCATCCAGATCTGGCGTGTGTTTGTATTTG	1684
RESULT 7			
ID	ADCC39221		
XX	ADCC39221 standard, cDNA, 1821 BP.		
XX	ADCC39221;		
XX	18-DEC-2003 (first entry)		
XX	Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.		
XX	ds; gene, antidiabetic; cytostratic; immunomodulatory; anorectic;		
KW	anti11pemic; nootropic; neuroprotective; immunostimulant;		
KW	anti1parksomian; anti-HIV; antischmatic; antiinflammatory; hypotensive;		
KW	antidiabeticosclerotic; hemostatic; osteopathic; gene therapy.; NOVX;		
KW	diabetes; obesity; cancer; lymphoma; uterine cancer; prostate cancer;		
KW	dyslipidemia; anorexia; wasting disorder; Alzheimer's disease;		
KW	Parkinson's disorder; cachexia; cardiomyopathy; AIDS; asthma;		
KW	Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;		
KW	hemophilia; graft-versus-host disease;		
XX	Albright hereditary osteodystrophy.		
XX	Homo sapiens.		
OS	XX		
FH	Key	Location/Qualifiers	
FT	CDS	73..1732	
FT		/*tag= a	
PN	WO2003010327-A2.		
XX	XX		
PD	06-FEB-2003.		
PF	02-MAY-2002; 2002WO-US014199.		
XX	XX		
PR	02-MAY-2001; 2001US-0288063P.		
PR	03-MAY-2001; 2001US-0288395P.		
PR	07-MAY-2001; 2001US-0289087P.		
PR	09-MAY-2001; 2001US-0289817P.		
PR	09-MAY-2001; 2001US-0289818P.		
PR	11-MAY-2001; 2001US-0290194P.		
PR	14-MAY-2001; 2001US-0290753P.		
PR	15-MAY-2001; 2001US-0291075P.		
PR	16-MAY-2001; 2001US-0291243P.		
PR	18-MAY-2001; 2001US-0292001P.		
PR	21-MAY-2001; 2001US-0292374P.		

QY	21	lyP-ProSerAspCyAspSerLysGluLeuGlnArgArgGlySerLeuAlaLeuPro	40
Db	133	AAACCCCTGGACCTGGACAGCAAGAGGCTGGAGCGCGCGCGAGAGCTGGCCCTGACC	192
QY	41	GlyLeuGlnGlyCysAlaGluLeuArgGlnGlyLeuSerLeuAspPheHisSerLeuCys	60
Db	193	GGGCTGCGAGGCTGCGCGAGGCTCCGCGAAGAGCTGTCCTTGAACCTTCACAGCTGTGT	252
QY	61	GluGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe	80
Db	253	GAGCAGACAGCCCATGGGTGGCCGCTCTTCCTGGACTTCCTCAAGTCCAGTCCACGGTTC	312
QY	81	ArgGlyAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro	100
Db	313	CGCAAGCGGCAACCTTCCTAAGGAGCGTCAAGACTGGAGCTGGCGCAGAGAGGAGACC	372
QY	101	ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	373	ACCAAAAGACGCGCTGGCAGGCGGCTGGTGGCCACTTGTGGAGTGCCTGCGCCGGGG	432
QY	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu	140
Db	433	AAACCGGACCCCTCTTACGCAAGGCGCTGGCCACCAATGCGCAAGCAGCAACACTAG	492
QY	141	GluGlnArgValAlaAlaValThrLeuArgValaGluAlaMetAlaPheLeuGlnGlu	160
Db	493	GAAAGGAGATGGCTGCGAGTACGCTGGCCAAAGGCTGAAGGCTTCTTTCGAAG	552
QY	161	GlnProPheLysAspPheValThrSerAlaPheLysAspLysPheLeuGlnTrpLysLeu	180
Db	553	CAGCCCTTTAAGGATTGGTACACAGCGCTTTCACACAACTTTCTGACGTGAACCTC	612
QY	181	PheGluMetGlnProValSerAspLysTrpPheThrGlnPheArgValLeuGlyLysGly	200
Db	613	TTGCAAGAGCAACCAATGTGCACAAAGTACTCACTCAAGTTCAGAGTCTGGGGAAAGGT	672
QY	201	GlyPheGlyGluValCysAlaValGlnValysAsnThrGlyLysMetTrpAlaCysLys	220
Db	673	GGTTTGGAGAGTATGTCGCTCGACTGAAACCACTGGAGAGATATGCTGCTGAAG	732
QY	221	LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGlnLys	240
Db	733	AAACTGGACAAAGACCGGCTGAAAGAAAGAGGCGCAAGAGATGGCTCTCTGAAAG	792
QY	241	GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGlnSer	260
Db	793	GAAATCTTGGAGAGAGTTCAGACGCTTCAATGTCTCTGCGCTAAGCTTGAAGAGC	852
QY	261	LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle	280
Db	853	AAGCCCATCTGCTGCTTGCATGAGCTGTGATGATGGGGAGACCTCAAGTTCCACATC	912
QY	281	TrpAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle	300
Db	913	TTCAACGTGGGACCGGCTGGCACTGACATGAGCGGGGTATCTTTAAGTGGCCAGATA	972
QY	301	AlaCysGlyMetLeuHisLeuHisGlyLeuGlyIleValTrpArgAspMetLysProGlu	320
Db	973	GGCTGTGGATGTGGACCTCATGAACCTCGGATCGTCAATCGGACAAGAGCCTTAG	1032
QY	321	AsnValIleLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu	340
Db	1033	AATGGCTTCTGGATGAACCTGGCACTGCAAGGTTATCTACCTGGGGCTGGCGTGGAG	1092
QY	341	MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTrpMetAlaProGlu	360
Db	1093	ATGAAGGATGGCAAGCCCATACCCAAAGGCGTGAACAAATGTTACAATGGCTCTGAG	1152
QY	361	IleLeuMetGluLysValaSerTrpSerTrpProValAspTrpPheAlaMetGlyCysSer	380
Db	1153	ATCCTAATGAAAGGTAAGTATTCCTATCCCTGTGGACGTGTTGCCATGGAGATGAGC	1212

QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1213 ATTATGAATGTTGGCTGACGAAACCATTAAGATTACAGAGAAAGAGTCACTAAA 1272
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1273 GAGATCTGAAAGCAAAAGACTCTGCAGAACAGAGGTCAATTCAGCATGATTACTTCA 1332
 QY 421 GluGluAlaLysAspLysCysArgPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1333 GAGGAAGCAAAAGATTATTCAGAGCTCTCTGCTTAAGAACAGAGCAACGCTTAGGA 1392
 QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrLysAsnPro 460
 Db 1393 AGCAGAGAAAGTCTGATGATCCAGAGAAACATCATTTCTTAAAGATCAACTTCTCT 1452
 QY 461 ArgLeuGlnAlaGlyLeuLysGluProPheValProAspProSerValValLysAla 480
 Db 1453 CCGCTGAGAGCTGGCTTAATGAACCCCACTTGGCCAGACCCCTTCACTGCTTTATGCC 1512
 QY 481 LysAspLysLeuAlaGluLysAspPheSerGluValArgGlyValGluPheAspLys 500
 Db 1513 AAAGACATCGCTGAATGATGATTTCTCTGAGGTTCCGAGGAGTGGATTTGATGACAA 1572
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProLysLeuGluGln 520
 Db 1573 GATAGAGATCTCTCAAAACCTTGGCAGAGGTGCTCTCTTACATGCGAGAGAA 1632
 QY 521 IleLeuGlnThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1633 ATTATGAAACGGACGCTTTGAGAACGATGATGACCCCAAGACGCTTACGGGTGTGAG 1692
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 Db 1693 GAGGTAATTCATCCAGTCTGCGCTGTGTTGTTATG 1731

RESULT 8
 ID AAH78799 standard, cDNA; 2249 BP.
 XX AAH78799;
 AC AAH78799;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human G-protein coupled receptor kinase 3 cDNA sequence.
 XX
 KW G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
 KW novel human protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200168869-A2.
 XX
 PD 20-SEP-2001.
 XX
 PE 08-MAR-2001; 2001WO-US007500.
 XX
 PR 10-MAR-2000; 2000US-0188449P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Walke DW, Wilganowski NL, Turner CA;
 DR WPI, 2001-570872/64.
 XX
 PT New polynucleotides encoding human proteins that share sequence
 PT similarity with animal kinases e.g. G-protein coupled receptor kinases,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 XX disorders.
 XX
 PS Disclosure; Page 33-34; 34pp, English.
 XX

CC The present cDNA sequence encodes a human G-protein coupled receptor
 CC kinase (GRK), also designated NRP (novel human protein) in the
 CC specification, which is shown in the sequence listing. The invention
 CC comprises novel human nucleotide and protein sequences. The invention
 CC provides similarity to G-protein coupled receptor kinases. Oligonucleotides
 CC derived from the nucleotides of the invention are useful as hybridisation
 CC probes for screening libraries and assessing gene expression patterns.
 CC The nucleotides of the invention are also useful in drug screening and
 CC gene therapy for the modulation of GRK expression. The nucleotides of the
 CC invention can be used to genetically engineer host cells to express GRK
 CC products in vivo. The nucleotide sequences of the invention are also
 CC useful in addressable arrays for identifying and characterising the
 CC temporal and tissue specific expression of the invention are also
 CC screen collections of genetic material from patients and in microarrays to
 CC particular medical condition. The proteins of the invention are useful
 CC for generating antibodies, as reagents in diagnostic assays, for
 CC identifying other cellular gene products related to GRK, and as reagents
 CC in assays for screening for compounds that are useful in the treatment of
 CC mental, biological or medical disorders/diseases

Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,166-281
 Score: 2883.00 Length: 2249
 Percent Similarity: 99.828 Matches: 552
 Best Local Similarity: 99.828 Mismatches: 1
 Query Match: 99.794 Indels: 0
 DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x AAH78799 (1-2249)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 354 ATGTGTGACATGAGGGGCGCTGCAACCTGATCGCAACCGCTTACCTGAGGCGCCG 413
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 414 AAGCCCTCGAGCTGCGACAGCAAGAGCTGACGGCGGGGTAGCTGCGCTGCGCC 473
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 474 GGGCTGACGGCTGCGCGAGCTTCCGACAGAGCTGCTTCACTTCCAGACCTGCTGT 533
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 534 GAGCAGCACCCATCGGTGCGCGCTCTTCCGTACTTCTTACCAAGTCCACAGCTTC 593
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
 Db 594 CGCAGAGCGGCAACCTTCTTCAAGAGAGCTGCAAGACTGGAGACTGCGAGAGAGACC 653
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 654 ACCAAGAGACAGCGGCTGCGAGGCTGGTGGCCACTTGGCAAGTGGCCCGCGG 713
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 714 AACCGCAACCTTCTTCAAGAGAGCTGCGAGGCTGCGCAAGTGGCAAGAGCACTAG 773
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
 Db 774 GAAAGCGAGTGGCTGCACTGACGCTGCGCAAGCTGAGGCGCATGCTTCTTGGCAAG 833
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 834 CAGCCCTTAAAGATTTCTGACCAAGCGCTTCTTCAAGAGTTCTGCAAGTGGCAACTC 893
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 894 TTCAGATGCAACCACTGTCAGAACAGTACTTCACTGATGTTCAAGATGCTGGGAAAGGT 953
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 85 ATGTGGACATGGGGGCGCTGGACAACTGATCGCCACACCGCTTACCTGGAGCGCCG 144
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 145 AAGCCCTCGACTCCGACAGCAAGAGCTGACGGCGCGCTGACCTGCGCCCTGCGCC 204
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnProHisSerLeuCys 60
 Db 205 GGGCTGACGGGCTGGCGGAGCTCGCCCAACACTGCTCCCTGAACTTCCACAGCGCTGT 264
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 265 GAGCAGAGCGCCCATCGCTGCGCGCTCTCTCGGACTTCTTACGACAGGCGCCACTTC 324
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTyrGluLeuAlaGluGlnPro 100
 Db 325 CGCAAGCGCGCAACTCTTCTTACAGAGAGCTGAGAACTGGAGCTGGCGAGAGAGAGCC 384
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 385 ACCAAAGACAGCGCGCTGAGGGGCTGGCGCGCTGCGCGCTGCGCGCGCGCGCG 444
 QY 121 AspProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 445 AACCCCGAACCTTCTCTTCAAGCAGCGCGCTGCGCAAGGCGCAAGCGCAAGCGCAAG 504
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaPheLeuGlnGlu 160
 Db 505 GAAAGACGAGTGGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 565 CAACCCCTTAAAGATTTCCGACAGCGCGCTTCTTCAAGAACTTTCGACGTGAACTC 624
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 625 TTCGAGATGCAACCAAGTGCAGACAACTCACTCACTCACTCACTCACTCACTCACTCA 684
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 685 GGTTTTGGGAGGTATGTCGCTCAGGTAAACACCTGGAGAGATGATGCTGCTGAG 744
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
 Db 745 AAACCTGGACAAAGCGGCTGAGAAAGAGGCGGAGAGATGCTCTCTTGGAGAAAG 804
 QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 Db 805 GAAATCTTGAGAAAGGTGACAGCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGAGC 864
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetGlnGlyLysAspLeuLysPheHisIle 280
 Db 865 AAGGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 925 TACACGTGGGACGCGGCTGACAGTACGCGGCTGATCTTTTACTTCGCGCCAGATA 984
 QY 301 AlaCysGlyMetLeuHisIleLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 985 GCTGTGGAGTGTGACCTCCATCACTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGAG 1044
 QY 321 AsnValIleLeuAspAspLeuGlyLysAsnArgLeuSerAspLeuGlyLeuAlaGlu 340
 Db 1045 AATGTGCTTCTGATGATCTCGGCACTGCGAGGTATTCGACTGGGCTGGCGCGGAG 1104
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1105 ATGAAGGGTGGCAAGCCCATCAAGAGGCTGAGAACCAATGGTACATGAGCTCTGAG 1164
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380

Db 1165 ATCTTAATGAAAAGATGATATTCCTATCCTGAGACGTGTTGCCATGGAGATGAGC 1224
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1225 ATTTATGAAATGTTGCTGAGCAACACCATTCAAATTAACAAGAAAGTCTGATAA 1284
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1285 GAGGATCTGAAGCAAAAGAACTTGCAGACAGAGGTCAAAATTCACATGATGAACTTCA 1344
 QY 421 GluGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1345 GAGAGAGAAAGATATTTGACAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 1404
 QY 441 SerArgGluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPro 460
 Db 1405 AGCAGAGAAAGTCTATGATATCCAGAAACATCATTTCTTTAAACGATCACTTCTCT 1464
 QY 461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValIleTyrAla 480
 Db 1465 CGCTGGAAGCTGCTTATGAAACCCCATTTTGTGCGAGACCTTCAAGTGTATGCTC 1524
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1525 AAAGACATCGCTGAAATGATGATTTCTGAGAGTTCGGGGGGTGAATTTATGACAA 1584
 QY 501 AspLysGlnPhePheLysAspPheAlaThrGlyValAlaValProIleAlaTyrGlnGlu 520
 Db 1585 GATAGCAGTCTTCAAAAATTTTGACAGAGTGTCTCTTATACATGACAGAGAA 1644
 QY 521 IleIleGlnThrGlyLeuPheGluGluLeuAspProAsnArgProThrGlyCysGlu 540
 Db 1645 ATTATGAAACCGGACTGTTTGAGAACTGAATGACCCCAACAGACTTACGAGTTGTAG 1704
 QY 541 GluGluLysSerSerLysSerGlyValCysLeuLeu 553
 Db 1705 GAGGTAATTCATCCAGTCTGCGGTGTGTATTG 1743

RESULT 10
 AAD28071 ID AAD28071 standard; cDNA; 1662 BP.
 AC XX
 DT 22-APR-2002 (first entry)
 XX XX
 DE Human Kinase cDNA.
 XX XX
 KW Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
 XX chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
 OS Homo sapiens.
 XX XX
 FT Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "Human kinase protein"
 XX XX
 EN W0200192496-A2.
 XX XX
 PD 06-DEC-2001.
 XX XX
 PF 31-MAY-2001; 2001WO-US017510.
 XX XX
 PR 01-JUN-2000; 2000US-0208331P.
 PR 18-DEC-2000; 2000US-00738894.
 XX XX
 PA (APPL-) APPLERA CORP.
 XX XX
 PI Guegler K, Di Francesco V, Beasley EM;
 DR WPI, 2002-13053/17.

DR P-PSDB: AAE17136.

XX New isolated human kinase proteins and nucleic acids, useful as a major
PT target for drug action and development, particularly for screening
PT modulators of the kinase peptides.

XX Claim 4; Fig 1; 87bp; English.

XX The invention relates to human kinase proteins that are related to G-
XX protein coupled receptor kinase subfamily. Human kinase gene is located
XX on chromosome 3. The kinase peptide and diagnostic compositions. The peptide
XX development of human therapeutic and diagnostic compositions. The peptide
XX is useful as a major target for drug action and development, and is
XX valuable to the field of pharmaceutical development to identify and
XX characterize modulators of the kinase. The proteins may also be used to
XX raise antibodies or to elicit an immune response, as a reagent in assays
XX designed to quantitatively determine levels of the protein in biological
XX fluids and as markers for tissues in which the corresponding protein is
XX preferentially expressed (either constitutively or at a particular stage
XX of tissue differentiation or development for providing a target for diagnosing a
XX disease or predisposition to disease mediated by the peptide. The nucleic
XX acid molecules are useful for probes, primers, chemical intermediates and
XX in biological assays. The nucleic acids are also useful in making vectors
XX containing the gene regulatory regions of the nucleic acid molecules and
XX for drug screening to identify compounds that modulate kinase nucleic
XX acid expression. The present sequence is human kinase cDNA expressed in
XX skins, germinal center B cells, colon, kidney and lung

XX Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other:

Alignment Scores:

Pred. No.: 3.9e-281 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: Gaps: 0

US-10-044-205a-2 (1-553) x AAD28071 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrValAlaThrLeuGlnAlaArg 20
DB 1 ATGTGTGACATGGGGGCGCTGACAACTGATCGCAACCGCTTACCTGACAGCCCG 60
QY 21 LysProSerAspCysAspSerLysGlnLeuGlnAArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCTCGGACTGGGACGACAAAGAGCTGACGGCGGGCTGAGCTGCGCCCTGCC 120
QY 41 GlysGlnGlnGlyValAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGACGAGGCTGCGGAGCTCGCCAAAGCTGTCCCTGAACCTTCCACGCTGTGT 180
QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCGACGACCCATCGGTGCGCGCTCTCCGACTTCTTACGACCAAGTCCACGCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAlaAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyPro 100
DB 241 CCGAAGCGGCGACCTCTTACAGGACGTGCAAACTGGAGAGCTGGCGAGAGGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAAGACAGGCGCTGACGGGCTGTGGCCACTTGTGCAAGTGCCTCGCCGAGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrTrpGln 140
DB 361 AACCCGCAACCTTCTTACGCGAGCGCGTGGCCACCAAGTGGACGACCACTGAG 420
QY 141 GlnGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGly 160
DB 421 GAAGAGCGAGTGGCTGACGTGACGTGGCCAAAGGCTGAGGCCATGGCTTCTTCAAGAG 480

QY 161 GlnProPheLysAspPheValThrSerAlaPheLysAspLysPheLeuGlnTrpLysLeu 180
DB 481 GAGCCCTTTAAGGATTTGTGACACGCGCTTTCACGCAAGTTCTGACGTGAACTC 540
QY 181 PheGlnMetGlnProValSerAspLysTrpPheThrGlnPheArgValLeuGlyLysGly 200
DB 541 TTCAGATGCAACAGTGTGACAACTGACTTCACTGAGTTCAGAGTGTGGGAAAGT 600
QY 201 GlyPheGlyLysValCysAlaValGlnValLysAsnTrpGlyLysMetLysAlaCysLys 220
DB 601 GCTTTGGGAGGTATGTCCCTCAGGTAAACCTGGAGAGTGTATCCCTGTAG 660
QY 221 LysLeuAspLysLysArgLysLysLysLysGlyGlyLysMetAlaLeuLeuGlnLys 240
DB 661 AAACGACCAAGAGGCGCTGAAAGAAAGGCGGAGAGAGTGCCTCTTGAAG 720
QY 241 GlnLeuLeuGlnLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGlnSer 260
DB 721 GAATCTTGGAGAGGTCAGCGACCTTTCATGTCTCTGGCTATGCTTGGAGAC 780
QY 261 LysThrLysLeuCysLeuValMetSerLeuMetAsnGlyLysAspLysPheHisLle 280
DB 781 AAGACCATCTCTCTCTTGTGATGAGCTGATGATGGGAGACTTCAAGTCCACATC 840
QY 281 TyrAsnValGlyThrArgLysLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
DB 841 TACACGTGGGACGCTGGCTGACATGAGCGGCTGATCTTTTACTCGGCGCAATA 900
QY 301 AlaCysGlyMetLeuHisLysLeuHisGlyLeuGlnGlyLysValThrArgAspMetLysProGln 320
DB 901 GCTGTGGAGTCTCACCTTCATGAACTCGCACTCGCATGCGGACATGAACTCGAG 960
QY 321 AsnValLeuLeuAspAspLeuGlnLysAsnCysArgLeuSerAspLeuGlyLeuAlaGln 340
DB 961 AATGCTCTTGTGAAGACCTCGACATCGAGTTATCTGACCTGGGCTGGCTGGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyLysMetAlaProGln 360
DB 1021 ATGAAGGAGTGGCAAGCCATCAACCAAGGCTGGAACATAGTTATCAATGCTCTCGAG 1080
QY 361 IleLeuMetGlnLysValSerTrpProValAspTrpPheAlaMetGlyCysSer 380
DB 1081 ATCTTAATGGGAAAGTAAATTTCTTATCTGAGCTGATGCTGGATGGAGTGAAGC 1140
QY 381 IleTrpGlnMetValAlaGlyArgThrProPheLysAspTrpLysGlnLysValSerLys 400
DB 1141 ATTATGAATGTTGCTGTGACGACCACTTGAAGATTCAAGAAAAGTCAAGTAA 1200
QY 401 GlnAspLeuLysGlnArgThrLeuGlnAspGlnValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGAAGCAAGAACTGCAAGACAGAGGTCAAAATTCAGCAATGATCACTTCA 1260
QY 421 GlnGlnAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAAGTATTTGACGCTCTTCTTGGCTTAAGAAACAGAGCAACGTTAGGA 1320
QY 441 SerArgLysLysSerAspAspProArgLysHisAspPheLysThrIleAsnPhePro 460
DB 1321 AGCAGGAAATCTGATGATCCAGGAAACATCACTTTTAAACATCACTTTTCT 1380
QY 461 ArgLeuGlnAlaGlyLeuIleGlnProPheValProAspProSerValValLysAla 480
DB 1381 CGCTGGAGACTGGCTTAATGAACCCCATTTGGCCAGACCTTCAAGTGTATTAGCC 1440
QY 481 LysAspLysLeuGlnLysAspPheSerGlnValArgGlyValGlnPheAspAspLys 500
DB 1441 AAAGACATGCTGAATTTGATGATTTCTGAGGTTGCGGGGAGTGAATTTGATGACAAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGln 520
DB 1501 GATTAAGCATTTTCAAACTTTGACAGAGTGTCTTATAGATGAGGAGAAATA 1560
QY 521 IleIleGlnThrGlyLeuPheGlnGlnLeuAsnAspProAsnArgProThrGlyCysGln 540

US-10-04-205A-2 (1-553) x AAS06702 (1-1662)

QY 1 MetValAspMetGlyAlaIleuAspSerLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20

Db 1 ArgSTGGACATGGGGGCGCTCGACCAACTGATGCGCAACACGCGCTACTCGACAGCGCCG 60

QY 21 LysProSerAspCysAspSerTyrSgluLeuGlnArgArgArgSerLeuAlaLeuPro 40

Db 61 AAGCGCTCGGACTCGACACGACCAAGACTGACGGGGCGCGCGCTACCGCTGGCGCTGCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnProPheHisSerLeuCys 60

Db 121 GGGCTCGACGGGCGTCCGGCGAGCTCCGCCAAGACTGTCTCCGACTTCCAGACGCTGTGT 180

QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80

Db 181 GAGCAGACGCCCATCCAGTCCGCGCTCTTCCTCCGACTTCTTCAAGCACAAGTCCACGCTTC 240

QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100

Db 241 CCGAAGCGGCGAACCCTTCCTGAGAGAGTGCAGAACTGGAGAGCTGGCGCAGAGAGGACCC 300

QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

Db 301 ACCAAGACAGCGCCCTCCAGGGGCTGGTGGCACTGTGCAGTGTCCCTCGCCCGGG 360

QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrTrpCysGlnAlaAlaThrThrGlu 140

Db 361 AACCGGCAACCTTCCTCCTGACGAGCGCGCGCGCACCAAGTCCAGACGACGACCACTGAG 420

QY 141 GluGlnArgValAlaAlaValaThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGlu 160

Db 421 GAAGAGCGAGTGGCTGCAGTGCAGCTGGCGCAAGGCTGAGGACCTTCCTTCGCAAGAG 480

QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180

Db 481 CAGCGCTTTAAGGATTTGCGACCAAGCCGCTTCAAGACAATTTCTGCAGTGGAACTC 540

QY 181 PheGlnMetGlnProValSerAspLysTrpPheThrGluPheArgValaLeuGlyLysGly 200

Db 541 TTGGAATGCCAACAGTGTCAAGAGTCACTCACTGAGTCAAGAGTCAAGGCTGGGAAAGCT 600

QY 201 GlyPheGlyGluValCysAlaValGlnValAsnThrGlyLysMetTyrAlaCysLys 220

Db 601 GGTTTTGGGAGGTATGTGCGCTCCAGGTAAAAACCTGGAAAGATGATCCCTGTAG 660

QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuGlnLys 240

Db 661 AAACCTGGACAAAGAGCGGTCAAGAAAGAGGCGGAGAAAGATGGCTCTTGGAAAG 720

QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260

Db 721 GAAATCTTGGAGAGGTACGAGCGCCCTTCAATGTCTCTCGGCTATACCTTGAAGG 780

QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280

Db 781 AAGACCATCTCGGCTGTCAAGAGCTGAGATGAGATGGGGGAGACCTCAAGTTCAATC 840

QY 281 TyrAsnValGlnThrArgGlyLeuAspMetSerArgValaIlePheTyrSerAlaGlnIle 300

Db 841 TACAACTGGGACCGCGGTGCGACAGAGACCGGGTGTCTTTATCTGGGCCAGATA 900

QY 301 AlaCysGlyMetLeuHisLeuHisGlyLeuGlyLleValTyrArgAspMetLysProGlu 320

Db 901 GCGTGTGGGCTGCGACCTCCATATCTCCGCACTGCTATACCGGACATGAGACCTGAG 960

QY 321 AsnValLeuLeuAspArgLeuGlyLysAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340

Db 961 AATGGGCTTGTGATGACCTCGGCAACCTGACAGGTTTCTGACTTGGGCGTGGCGTGGAG 1020

Db 1021 ATGAAAGGTGGCAAGCCATCAACCAAGGCTGAAACCAATGTTATCATGCTCTCTAG 1080
 QY 361 TLeuMetGluValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGAAAGAGTAAATATTCCTATCTGTAATCTGTTGCTTGCATGGATGACAG 1140
 QY 381 TLeuGluMetValAlaGlyArgThrProPheLeuAspTyrTyrGluValSerTyr 400
 Db 1141 ATTATGAATGTTGCTGACGACACCATTTCAAAATTAACAGAAAGGTCAGTAA 1200
 QY 401 GluAspLeuValGlnArgThrLeuGlnAspGluValValSerGlnHisAspAsnPheThr 420
 Db 1201 GAGACTCTGAACCAAGAACTGCAAGACGAGGTCAAATTCAGATGATTAATTCACA 1260
 QY 421 GlnGluAlaValAspTyrLeuArgLeuPheLeuAlaValSerProGlnGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATATTTGAGGCTCTTCTTGCTTAAAGAACAGAGCAACGCTTAA 1320
 QY 441 SerArgGluValSerAspAspProArgTyrHisHisPhePheLeuThrTyrLeuPhePro 460
 Db 1321 AGCAGAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTAAACGATCAACTTCTT 1380
 QY 461 ArgLeuGluAlaGlyLeuLeuGluProPheValProAspProSerValValTyrAla 480
 Db 1381 CCCTCGAAGCTGGCTTATGAAACCCCATTTGCGCAACCTTCAAGTGTATTATGCC 1440
 QY 481 LysAspTyrLeuAlaGluLeuAspAspPheSerGluValArgGlyValGluPheAspTyr 500
 Db 1441 AATAGCATCTCGTAAATGATGATTTCTGAGAGTTCCGGGGGAGGAAATTTGATGACAAA 1500
 QY 501 AspLysGluPhePheLeuAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGlu 520
 Db 1501 GATAAGCACTTCTTCAAAACTTTCGACAGGCTGCTTCTATAGCATGGCAAGAA 1560
 QY 521 TLeuGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATGAAACGAGACGTTTGAAGACGATGACCCCAACAGCTTACGGGTTGTAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCCAAAGTCTGCGTGTGTTGTTATTTG 1659
 RESULT 12
 ACC44826
 ID ACC44826 standard; cDNA, 1662 BP.
 AC ACC44826;
 DT 04-JUN-2003 (first entry)
 XX Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
 XX Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;
 XX neuroprotective; nootropic; cardioprotective; anti-Parkinsonian; cardiant;
 XX vasodilator; antihypertensive; gene therapy; cancer; diabetes; CNS disorder;
 XX central nervous system disorder; cardiovascular disorder; asthma; COPD;
 XX chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
 XX Alzheimer's disease; Parkinson's disease; congestive heart failure;
 XX myocardial infarction; ischemic disease; hypertensive vascular disease;
 XX gene; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 1..1662
 XX FT /*tag= a
 XX product= "G protein-coupled receptor kinase (GRK)"
 XX W02003018815-A2.
 XX 06-MAR-2003.
 XX 19-AUG-2002; 2002MO-EP009235.

XX 21-AUG-2001; 2001US-0313464P.
 PR (FARB) BAYER AG.
 XX xiao Y;
 XX WPI: 2003-278669/27.
 DR P-PSDB; ABP96707.
 XX New G-protein coupled receptor kinase polypeptides and polynucleotides,
 PT useful in identifying modulators of the enzyme for treating cancer,
 PT diabetes, a central nervous system disorder, a cardiovascular disorder or
 PT asthma.
 XX Claim 1; Fig 1; 129pp; English.
 PS The present sequence encodes a human G protein-coupled receptor kinase
 CC (GRK) protein (1). (1) has cytosolic, antidiabetic, neuroprotective,
 CC nootropic, cardioprotective, anti-Parkinsonian, cardiant, vasodilator and
 CC antihypertensive activities, and can be used in gene therapy. (1) can be
 CC regulated to treat cancer, diabetes, a central nervous system (CNS)
 CC disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
 CC Parkinson's disease), cardiovascular disorders (e.g. congestive heart
 CC failure, myocardial infarction, ischemic diseases of the heart or
 CC hyperensive vascular diseases), asthma and chronic obstructive pulmonary
 CC disorder (COPD). GRK molecules are useful in screening for agents that
 CC regulate or decrease the activity of a GRK. GRK sequences may also be used
 CC for detecting diseases and abnormalities or susceptibility to diseases
 CC and abnormalities related to the presence of mutations in the nucleic
 CC acid sequences that encode the GRK enzyme
 XX
 SQ Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,52e-280 Length: 1662
 Score: 2868.00 Matches: 550
 Percent Similarity: 99.46% Conservative: 0
 Best Local Similarity: 99.46% Mismatches: 3
 Query Match: 99.27% Indels: 0
 DB: Gaps: 0
 US-10-044-205a-2 (1-553) x ACC44826 (1-1662)
 QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaThrAlaTyrGlnAlaArg 20
 Db 1 ATGTGTGACATGGGCGCTGCGGACCTGATGACCAACCGGCTTACCTGAGGCGCGG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 61 AAGCCCTCGACCTGCAACAGCAAGAGCTGACAGCGGCGGCGGCTGACCTGCGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnValLeuSerLeuAsnPheHisSerLeuCys 60
 Db 121 GAGGCTGACGCGCTGCGGAGCTCGGCAAGACTTCTTCAATCTTCCACACCTGCT 180
 QY 61 GlnGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GACACAGCGCCATCGTGTGCGCTCTTCCGTACTTCTTCCAGCAGTGGCCACAGTTC 240
 QY 81 ArgValAlaAlaThrPheLeuGluAspValGlnAsnTyrGluLeuAlaGluGluGlyPro 100
 Db 241 CGCAAGCGGCAACTTCTTCAAGAGCGTGAAGCTGAGCTGCGGAGGAGAGCC 300
 QY 101 ThrTyrAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGGCGCTGCGGAGCTGCGGCACTTGTGCAATGCTTCCCTGCGCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrTyrCysGlnAlaAlaThrThrGlu 140
 Db 361 AAGCCGACCTTCTTCTGAGCGGCGCTGCGGCAAGAGCCAGAGCCACCACTGAG 420
 QY 141 GlnGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160

D	421	GAAGAGGAGTGGCTGACGTGACGCTGAGCCATGGCCATTCCTTTCGCAAGG	480
Q	161	GLnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu	180
D	481	CAGCCCTTTTAAAGATTTTCGTGACCAACGCCCTTCTCAACAATTTTCGACGTGGAACTC	540
Q	181	PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly	200
D	541	TTTGAGATTCACAACGAGTGTAGACAAAGTACTCACTGAGTCTCAAGAGCTGGGGAAAGGT	600
Q	201	GLPheGlyGlyValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys	220
D	601	GGTTTGGGGAGGTAACTGGCCCTCAAGGTGAAACACATCGGAAGATGATCCCTGTAAG	660
Q	221	LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys	240
D	661	AAATCTGCACAAAGAGGCTGAAAGAAAGGGTGGCGAAGATGGCTCTCTGGAAGG	720
Q	241	GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer	260
D	721	GAATCTTGGAGAAAGGTCAAGGCCCTTTTCAATTGCTCTCGGCTCAATCCCTTGAAGG	780
Q	261	LysThrIleIleuCysLeuValMetSerLeuMetAsnGlyGlyAspLysLysPheIle	280
D	781	AAAGCCCATCTCGGCTTGTGATGAGCTGATGAATGGGGAAACCTCAAGTCCATATC	840
Q	281	TyrAsnValGlyTyrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle	300
D	841	TTCAACTCTGGCACCGGTGGCTTGACAAAGACCGGCTGTATCTTTTATCTGGGCCAAGTA	900
Q	301	AlaCysGlyMetLeuHleLeuHleGlnLeuGlyIleValTyrArgAspMetLysProGln	320
D	901	GCGTGTGGAGTCTGCACCTTCATGAACTGGCAATGGCTCAATGGAACTGAAGCTGAG	960
Q	321	AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGln	340
D	961	AATGGCTCTTGATGATGACTCGGCAATCGAGGTATCTGACCTTGGGGCTGGCGTGAGG	1020
Q	341	MetLysGlyGlyLysProIleThrGlnArgAlaGlyTyrAsnGlyTyrMetAlaProGln	360
D	1021	ATGAAAGGTGGCAAGCCATCAACCAAGGGCTGGAAACCAATGGTTCAATGGCTCTTAG	1080
Q	361	IleLeuMetGlnLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer	380
D	1081	ATCCTAATGAAAAAGTAATTTATTCCTTTCCTGAGCTGGTGGTGCATGGGATGAGC	1140
Q	381	IleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGlyLysValSerLys	400
D	1141	ATTATGAAATGGTTGCTGGACGAACAACATTCAAGATTCAAAGGAAAGGTCTGTAAG	1200
Q	401	GluAspLeuLysGlnArgThrLeuGlnAspGlyValLysPheGlnIleAspAsnPheThr	420
D	1201	GAGGATCTGAAGCAAAAGAACTTGCAGAAAGAGTCAAAATTCAGCATATTACTTACA	1260
Q	421	GlnGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly	440
D	1261	GAGCAAGCAAAAGATTTTGGAGGCTCTTCTTGGCTTAAAGAAACAAAGACACGCTTAAG	1320
Q	441	SerArgGlnLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro	460
D	1321	AGCAGAAAGAAAGCTGAGATGCCACGGAACATCATTTCTTAAACGATCAACTTTCCT	1380
Q	461	ArgLeuGlnAlaGlyLeuIleGlnProProPheValProAspProSerValValTyrAla	480
D	1381	CGCTGGAAAGCTGGCTTAATTGAACCCCATTTGGCCAGACCCCTTCAAGTGTATGCC	1440
Q	481	LysAspIleAlaGlnIleAspAspPheSerGlyValArgGlyValGlnPheAspAspLys	500
D	1441	AAAGACATCGCTGAATTTGATTTCTCTGAGGTTGGGGGTGGAAATTTGATGACAA	1500
Q	501	AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGlnGln	520

Db	1501	GATTAAGCAAGTCTTCAAAAACCTTTCGGACAGGTGCTGCTTCTTAATGACATGGCAGGAAGA	1560
Qy	521	lellleqlurhrglyleupheglugluileusnapProbsnaripProthrglyCysglu	540
Db	1561	ATTATAGAAACGGGAGCTTTGAGGAACTGAAATATACCCCAAGACACTACGGGTTGTAG	1620
Qy	541	GIUGIYanserSerlyesSerglyValCysleudeu	553
Db	1621	GAGGGTAAATTCATCCAACTGCGCGTGTGTTGTATTG	1659
RESULT 13			
ID	AAD46351		
XX	AAD46351	standard; cDNA, 1486 BP.	
AC	AAD46351;		
XX			
DT	27-JAN-2003	(first entry)	
XX			
DE	Human cone opsin kinase (GRK7) OK6 splice variant cDNA.		
KM	Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;		
KM	GRK7; cone visual signalling; visual sensitivity; visual resolution;		
KM	night blindness; colour blindness; Oguchi disease; pineal gland activity;		
KM	chronobiological desynchrony; depression; anxiety; memory loss; headache;		
KM	menal foginess; fatigue; jet lag; circadian rhythm; ophthalmological;		
KW	gene therapy; antidepressant; analgesic; gene; ds.		
XX			
OS	Homo sapiens.		
Key	Location/Qualifiers		
FT	1..1062		
FT	/*tag= a		
CD	/product= "human GRK7 OK6 splice variant protein"		
PN	MO200272541-A2.		
XX			
PD	19-SEP-2002.		
XX			
FF	07-MAR-2002; 2002MO-US007025.		
XX			
PR	07-MAR-2001; 2001US-0274066P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
PI	Bird TA, Spencer M, Mosley BA;		
DR	WPI: 2002-122307/78.		
DR	P-PSDB; MME28953.		
XX			
PT	Identifying compounds that alter inhibition of cone opsin kinase		
PT	polypeptide activity for treating a conditions related to cone visual		
PT	signaling, comprises mixing a compound with a cone opsin kinase and with		
PT	an inhibitory polypeptide.		
PS	Example 4; Page 48-49; 61pp; English.		
XX			
CC	The present invention relates to novel human cone opsin kinase (G-protein		
CC	coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.		
CC	The invention further relates to a method of identifying compounds that		
CC	alter the inhibition of GRK7 polypeptide activity which involves mixing a		
CC	test compound with GRK7 protein and an inhibitory polypeptide and		
CC	determining if the test compound alters the inhibition of GRK7 protein		
CC	activity by the inhibitory polypeptide. GRK7 sequences are useful for		
CC	treating conditions related to cone visual signalling (e.g., night		
CC	blindness, colour blindness, difficulty with colour vision, visual		
CC	sensitivity, visual resolution or in adapting to changes in light		
CC	intensity, Oguchi disease or dominant congenital stationary night		
CC	blindness), pineal gland activity (e.g., chronobiological desynchrony,		
CC	depression, anxiety, mental foginess, memory loss, headaches, fatigue,		
CC	or jet lag). Agonists of GRK7 polypeptide activity may be used to treat		
CC	or ameliorate symptoms of a disease for which increased GRK7 polypeptide		
CC	activity is beneficial, e.g., decreased colour sensitivity or other cone		
CC	photoreceptor-mediated diseases. The GRK7 proteins are also		

CC preparation of a medication for treating a condition or disease related
 CC to cone photoreceptor visual signaling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for
 CC individuals with such disorders. The present sequence is human GRK7 OK6
 CC splice variant cDNA

XX Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	1.74e-225	1486	460	0	1	1
Percent Similarity:	2326.00					
Best Local Similarity:	83.03%					
Query Match:	80.51%					

US-10-044-205a-2 (1-553) x AAD46351 (1-1486)

QY 1 MetValAspMetGlyValAlaLeuAspAsnLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGGTGGACATGGGGGCGCTTGGACAACTGATGGCAACCGCTTACCTGCGAGCGCCGG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnAlaArgAlaGlyGlySerLeuAlaLeuPro 40
 Db 61 AAGCCCTTGGACCTGGACAGCAAGAGCTGCAAGCGCGCGCTGAGCTTGGCTGGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnProLeuHisSerLeuCys 60
 Db 121 GGGCTGGACGGCTGGCGGAGCTCGCGCAAGCTGTCTCTGAACTTCCGACACCTGGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGACGCCCATGGTGGCGCTCTTCCGTGATCTCTTCCGACAGCGCCCAAGCTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGluGlnGlyPro 100
 Db 241 CGGAGGGCGGACCTTCTTCAAGAGCGTGGCAAGCTGGAGCTGGAGAGGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGCGCGCTCGAGGGCTGGTGGCACTTGTCCAGTGGCTCCCGCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140
 Db 361 AACCCTGCAACCTCTCTTCAAGCGCGCTGGCAAGAGCGCAAGCGCCACCACTGAG 420
 QY 141 GluGlnArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnLys 160
 Db 421 GAGAGCGAGTGGCTGGAGCGCTGGCCAGCGCTGAGCGCTGAGCGCTTCTTGGAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTTAAGGATTTCTGACAGCGCTTCTTACGACAAAGTTTCTGGAGGAGAACTC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuLysGly 200
 Db 541 TTCGAGATGCAACCATGTCAGACAGATCTTCACTGAGTTCAAGAGTCTGGAGAAAGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGATGTCCGCTCAGGTAAAAACAGTGGAGAGATGATGCTGTAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGlnLys 240
 Db 661 AAACCTGGCAAGAGCGCTGAGAGAGAAAGCTGGGAGAGATGCTCTTGGAGAAAG 720
 QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAATCTTGGAGAGAGCTCAGCAGCCCTTCACTGTCTCTGCGCTTGGAGAGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetSerLysGlyLysAspLeuLysPheHisIle 280

Db 781 AAGACCATCTCGCTTGTGATGAGCGCTGATGATGGGGAGAGCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACAACTGGGACCGCGTGGCTGACATGAGCCGGGTGATCTTTACTCGGCCCAAGTA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGln 320
 Db 901 GCGTGTGGAGTGGCTGCACTTCATGAACTGGCATGTCTATGGGACATGAAAGCTTGG 960
 QY 321 AsnValLeuLeuAspSerLeuGlyLysCysArgLeuSerAspLeuGlyLeuAlaValGln 340
 Db 961 AATGTCTTCTGATGATCACTGGGCAACGCAAGTTATCTGACCTGGGGCTGGCGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGln 360
 Db 1021 ATGAAGGGTGGCAAGCCCATCACCCG----- 1047
 QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1047 ----- 1047
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1047 ----- 1047
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1047 ----- 1047
 QY 421 GluGlnAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1047 ----- 1047
 QY 441 SerArg-GluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPhePr 460
 Db 1048 ---AGAGAAAGCTGATGATCCAGAGAAACATCATTTCTTAAACGATCACTTCC 1104
 QY 460 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValTyrAla 480
 Db 1105 TCGCTCGAAGCTGGCTTATTTGAACCCCATTTGTCCAGACCTTCAAGTGTATTAGC 1164
 QY 480 AlaAspLysAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1165 CAAGAACATGCGGAAATTGATTTCTCTGAGGTTGGGGGGTGGAAATTGATGACAA 1224
 QY 500 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlnG 520
 Db 1225 AGATTAGCAGTTCTTCAAAACTTTGCGACAGGTGCTGTTCTTATGACATGGCAGGA 1284
 QY 520 uIleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysG 540
 Db 1285 AATTATGAAACGGGACGTGTTGAGAGACTGATGACCCCAACAGACTACGGGTTGTGA 1344
 QY 540 uGluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1345 GAGGGTATTATCATCAAGCTGGCGTGTGTGTATTG 1384

RESULT 14

ABZ56934 standard; DNA; 1191 BP.

AC ABZ56934;

DT 04-APR-2003 (first entry)

DE Human RGSN09 encoding DNA # SEQ ID 2.

KW Human; RGSN09; heart disease; cancer; omentopathy; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

[illegible]

XX 08-MAR-2001; 2001MO-US007500.
 PF 10-MAR-2000; 2000US-0188449P.
 PR
 XX (LEXI-) LEXICON GENETICS INC.
 PA
 XX Walke DW, Wilganowski NL, Turner CA;
 F1
 XX WPI; 2001-570872/64.
 DR P-SDB; AAG77816.
 XX
 XX New polynucleotides encoding human proteins that share sequence
 PT similarity with animal kinases e.g. G-protein coupled receptor kinases,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 XX Claim 4; Page 32; 34pp; English.
 PS
 XX The present cDNA sequence encodes a human G-protein coupled receptor
 CC Kinase (GRK), also designated NRP (novel human protein) in the
 CC specification, which is claimed in the invention. The invention comprises
 CC novel human nucleotide and protein sequences which have similarity to G-
 CC protein coupled receptor kinases. Oligonucleotides derived from the
 CC nucleotides of the invention are useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns. The
 CC nucleotides of the invention are also useful in drug screening and gene
 CC therapy for the modulation of GRK expression. The nucleotides of the
 CC invention can be used to genetically engineer host cells to express GRK
 CC products in vivo. The nucleotide sequences of the invention are also
 CC useful in addressable arrays for identifying and characterising the
 CC temporal and tissue specific expression of a gene and in microarrays to
 CC screen collections of genetic material from patients who have a
 CC particular medical condition. The proteins of the invention are useful
 CC for generating antibodies, as reagents in diagnostic assays, for
 CC identifying other cellular gene products related to GRK, and as reagents
 CC in assays for screening for compounds that are useful in the treatment of
 CC mental, biological or medical disorders/diseases
 XX
 XX Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1.67e-172 Length: 1062
 Score: 1801.00 Matches: 349
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 62.34% Indels: 0
 DB: Gaps: 4
 US-10-044-205a-2 (1-553) x AAH78798 (1-1062)
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 DB 1 ATGGTGACATGGGGGCTCTGGACACCTTAATGCCAACACCGCTACCTGCAGGCCGG 60
 QY 21 LysProSerAspCysAspSerIleGlnLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCCTGAGCTGCGACAGCAAGAGCTGACGGCGCGCGCTGACCTGCGCTGCCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnIleLeuSerLeuAsnPheHisSerLeuCys 60
 DB 121 GGGCTGCGAGGCTGCGCGAGCTCGCGCAAGCTGTCTTGAACCTTCCACAGCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCCATGGTGGCGCTCTTCCGTGACTCTTACGCCACAGTGCACAGTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTyrGlnLeuAlaGlnGlnGlyPro 100
 DB 241 CGCAAGCGCGCACTTCTCTTAAGAGCGTGAAGAACTGGAGCTGGCGAGGAGGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

DB 301 ACCAAAGACAGCCGCTGCGAGGCTGTGGCCACTTGTGAGATGCCCTGCCCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrIleCysGlnAlaAlaThrGln 140
 DB 361 AACCCGCAACCTTCTCTGACAGCGCGTGGCCACCAAGTGCAGAGCCACACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgIleAlaGluAlaMetAlaPheLeuGln 160
 DB 421 GAAGAGCAGTGGCTGCGAGTGAAGCTGCGCAAGCTGAGGCCATGCGCTTCTTGCAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 DB 481 CAGCCCTTAAAGATTTCTGTGACAGCCCTTACAGCAAGATTCTGCAAGTGAATC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGlnPheArgValAlaLeuGlnGly 200
 DB 541 TTGAGATGCAACCAAGTGCAGCAAGATCTTCACTGAGTGCAGTGTGGGAAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 DB 601 GATTTGGGAGATATGTGCTGCAGGTGAAACACTGGGAGATGTATGCTGTAAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlnLysMetAlaLeuLeuGlnLys 240
 DB 661 AATCTGCAAGAACCGCTGAAAGAAAGGTGGCAGAAAGATGCTCTTGGAAAG 720
 QY 241 GluIleLeuGlnLysValSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 DB 721 GAATCTTGAAGAGTGCAGAGCCCTTCACTGTCTCTGCTTATGCTTGTGAGAC 780
 QY 261 LysThrIleLeuCysLeuValMetSerLeuMetLeuGlyLysPheLysPheHisIle 280
 DB 781 AAGCCCATCTGCTGCTGTATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 841 TCAACGTGGGACGCGTGGCTGACATGACCGCGTGAATCTTTATCTGGCCAGATA 900
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 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlnAlaValGln 340
 DB 961 AATGTCTTCTGATGATGACTCTGGAATCTGCAAGTTATCTGACCTGGGCTGGCGTGGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArg 350
 DB 1021 ATGAAGGTGGCAAGCCCATCAACCAAGAG 1050

Search completed: August 13, 2004, 19:14:24
 Job time : 481 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 13, 2004, 18:42:11 ; Search time 2705 Seconds

(without alignments)
6104.912 Million cell updates/sec

Title: US-10-044-205A-2
Perfect score: 2889
Sequence: 1 MWMGALDNLANTAYLQAR.....NRPTGEBGSSKSVCLL 553

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/CGN2 I/USPTO spool/US10044205/runat_06082004_104322_23369/app query.fasta_1.711
-DB=EST -OPMT=fastop -SURFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-NOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPM=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044205 @CGN 1.1 2607 @runat_06082004_104322_23369 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estda:*
2: em_esthm:*
3: em_estin:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262	43.7	2329	11	BC027597 Homo sapi
2	1219.5	42.2	2989	11	BC057206 Mus muscu
3	1218.5	42.2	2978	11	AK051405 Mus muscu
4	955.5	33.1	1721	29	AY406080 Homo sapi
5	940.5	32.6	1721	29	AY406082 Mus muscu
6	883.5	30.6	1201	13	EX404586 BX404586
7	826.5	28.5	968	13	BQ066445 AGENCOURT
8	822.5	28.5	998	13	BQ057613 AGENCOURT
9	813.5	28.2	1017	13	BQ061150 AGENCOURT
10	803.5	27.8	1019	13	BQ061148 AGENCOURT
11	796.5	27.6	1028	13	BQ063841 AGENCOURT
12	793	27.4	934	13	BQ057469 AGENCOURT
13	793	27.4	1058	13	BQ057469 AGENCOURT
14	791.5	27.4	917	13	EX849055 BX849055
15	787	27.2	838	13	EX849055 BX849055
16	782.5	27.1	769	13	BQ056240 AGENCOURT
17	780	27.0	995	13	BQ056240 AGENCOURT
18	767.5	26.6	903	13	BQ056240 AGENCOURT
19	762.5	26.4	792	13	BQ056240 AGENCOURT
20	761	26.3	988	13	BQ066396 AGENCOURT
21	752	26.0	810	13	BQ066396 AGENCOURT
22	747.5	25.9	851	13	BQ030423 AGENCOURT
23	740.5	25.6	990	13	BQ071614 AGENCOURT
24	737.5	25.5	724	13	BQ071614 AGENCOURT
25	737.5	25.5	857	13	BQ052789 AGENCOURT
26	737.5	25.5	1002	13	BQ065277 AGENCOURT
27	737	25.5	937	12	BQ477593 AGENCOURT
28	731.5	25.3	660	13	BQ052019 AGENCOURT
29	731.5	25.3	1622	29	AY406081 AGENCOURT
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32	728.5	25.2	1796	8	BC021221 Homo sapi
33	720.5	24.9	765	9	AJ442768 AGENCOURT
34	717.5	24.8	815	9	AJ442768 AGENCOURT
35	712.5	24.7	984	13	BQ055527 AGENCOURT
36	702.5	24.3	1057	13	BQ071329 AGENCOURT
37	700.5	24.2	696	10	BE677821 AGENCOURT
38	700	24.2	906	14	CB195708 AGENCOURT
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41	686.5	24.1	1067	12	BM927442 AGENCOURT
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45	681	23.6	1032	12	BM472080 AGENCOURT

ALIGNMENTS

RESULT 1
BC027597
LOCUS
DEFINITION
BC027597
ACCESSION
BC027597
VERSION
BC027597.1
KEYWORDS
HTC
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2329)

FEATURES

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source
Location/Qualifiers
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/tissue_type="spinal ganglion"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
256..1893
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ORIGIN

homolog [Mus musculus] (SWISSPROT|O70293, evidence: FASTA,
100%ID, 96.9%length, match=1714)
putative"

Alignment Scores:

Read, NO.:	2,888-112	Length:	2978
Score:	1218.50	Matches:	236
Percent Similarity:	67.20%	Conservative:	102
Best Local Similarity:	46.99%	Mismatches:	153
Query Match:	42.18%	Indels:	12
DB:	11	Gaps:	6

03-10-044-205A-2 (1-553) X AK051405 (1-2978,

[illegible][illegible]

Db	561	GTTCGGGCGACCTGGTAAATGATGTCCTGTGTAACGCTTGAGAAAGAGAGATCAAAAG	620
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Db	621	AGGAAAGGCGAATCGATGGCACTCAAGAAAGCAATGTTCTTGAGAAAGGTCAACAGCCAG	680
Qy	250	Phel1eValSerLeuAlaTyrAlaPheGluSerIlyThrHsIleuCySLeuValMetSer	269
Db	681	TTTGAGTCAACCTGGCGCTATGCTATGAAACCAAGATGACATGCTGCTGGTTTGACC	740
Qy	270	LeuMetAngIyGLIYAspPheIlyPheHisIleTyrAsnValGIYThrArgIYLeuAsp	289
Db	741	ATTATGATGGTGGTACCTGATGATTTTCACATCTCAATTCATATGAGGAAATCCGGCTTGAG	800
Qy	290	MetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlu	309
Db	801	GAAAGCGAAGCTTATTTATTTATGACGTGAGATCCCTGTGGCTTAAGACTTACACCTT	860
Qy	310	LeuGlyIleValTyrArgAspMetIlySPROGluAsnValLeuLeuAspAspLeuGIYAsn	329
Db	861	GAGAACCTCTCTATGAGATCTAAACCCGAAACATCTTGCTGGATGATTAATGCGCAC	920
Qy	330	CysArgLeuSerAspLeuGIYLeuAlaValGIYMetIyGLIYLYSPROilethrgin	349
Db	921	ATAAGATCTCGAAGCTCGAGCTGGCGGTGAAGATCCCGAGAGAGACTTATCCGTGAC	980
Qy	350	ArgAlaGIYThrAsnGIYTYrMetAlaPROGluIleLeuMetGluIlyValSerTYrSer	369
Db	981	CGGGTAGGCACTGTGGCTCATGGCCCAAGCTTGAACACACAG--CGANTGGA	1037
Qy	370	TyrProValAspTPheAlaMetGIYCySserIleTYrGluMetValAlaGIYArgThr	389
Db	1038	CTGAGCGCTGACATCTGGCGCTGGCGCTGCTCATGATGATGAGATGTAAGGCCATGCA	1097
Qy	390	ProPheIlyAspTYrIlySGIYLYSValSerIyGluAspLeuIySGIYAlaTYrLeuGln	409
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Qy	410	AspGIYValIlySPheGlnHisAspAsnPheThrGIYAlaIlyAspIleCysArgLeu	429
Db	1158	ACTGAGGAAGTATATTC--TCCAGTCTCTGAAAGAGGCCCAAGTCCATGCAACATG	1214
Qy	430	PheLeuAlaIlySPeProGluIlyArgLeuGIYSerAlaGIYLYS--SerAspAsp	448
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Qy	449	ArgIlyShiShiSPhePheIlyThrIleAsnPhePROArgLeuGluAlaIleuIleGlu	468
Db	1275	AAGAGGCAACCTTTCTTCAGGAACATGAACCTTTAAGGCCCTGAGAGGCTGGAGTGTGGAT	1334
Qy	469	ProProPheValPProAsp	474
Db	1335	CTCTCCCTTCCTTCAGAT	1352
RESULT 6			
LOCUS	EX404586/c	1201 bp	mRNA
DEFINITION	BSX04586 Homo sapiens NEUROBLASTOMA		linear EST 13-MAY-2003
ACCESSION	CGD00484X005 3-PRIME, mRNA sequence.		
VERSION	EX404586		
KEYWORDS	EX404586.1 GI:30648023		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Euteleia; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (Dases I to 1201)		
TITLE	Li,W.B., Gruber,C., Jesse,J. and Polayer,D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	Contact: Genoscope		

Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A004AG03NP1&cluster=3090.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0A004AG03NP1.

FEATURES

source

Location/Qualifiers
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/db_xref="taxon:9606"
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/note="Vector: PCWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the PCWSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 8,966-79 Length: 1201
Score: 883.50 Matches: 166
Percent Similarity: 74.59% Conservative: 75
Best Local Similarity: 54.07% Mismatches: 3
Query Match: 30.58% Indels: 3
DB: 13 Gaps: 3

US-10-044-205a-2 (1-553) x BX40586 (1-1201)

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195 ArgValLeuGlyValGlyPheGlyGlyValAlaValGlnValLysAsnThrGly 214
943 CGAGTCTCGGCGAAAGGTGCTTTGGGAGGTGTGGCGCTGCGAGTGCAGGCTCAGGT 884
215 LysMetTyrAlaCysIleLysLeuAspLysLysLysLysLysLysLysLysLys 234
883 AAGATTGATGCTCGAAGAAAGTGAAGAAAAGCGATCAAGACGGAAGGAGGCGCC 824
235 MetAlaLeuLeuGlyValGlyLeuGlyValSerSerProPheIleValSerLeu 254
823 ATGGCGCTGAACGAGACGATCCGAGAAAGTGAACGATGTTGTAGTGAAGCTTG 764
255 AlaTyrAlaPheGlySerLysThrLsLeuCysLeuValMetSerLeuMetAsnGly 274
763 GCCTACGCTGATGAACGAGACGCGCTGCTGCGTGGTGTGACACATGATGAAGCGG 704
275 AspLeuLysPheHisIleTyrAsnValGlyThrArgLysLeuAspMetSerValIle 294
703 GACCTCAAGTTCACATCTACCATGAGCGAGCTGCTTCCCGAAGCGGAGCGCTC 644
295 PheTyrSerLysIleLeuAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleVal 314
643 TTCACAGCGCCGAGATCGCTGCTGCTGAGAGACCTGCAACCGGAGCGCATCTG 584
315 ArgAspMetLysProGlnAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSer 334
583 AAGGACCTGAAGCCGAGAACTCTGCTGAGTGAACACGCGCACATCCGCACTCTAC 524
335 LeuGlyLeuAlaValGluMetLysGlyLysPheProIleThrGlnArgAlaGlyHis 354
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463 GGTACATGCTCGGAGGTGTGTAAGATGAA----CGTTACAGCTTACGCTGACTGG 407

375 PheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyr 394
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395 LysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPhe 414
346 AAGAGAAAGTTCAGCGGAGAGAGCTG---GAGCGGCTGCTGAGAGAGGTCCCGAGAG 290
415 GlnHisAspAspPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLys 434
289 TATTCGAGCGCTTTCCCGCAGCGCCGCTCATCTTGTCTCAGCTCTCTGCAAGGAC 220
435 ProGluGlnArgLeuGlySerArgGlyLysSer---AspAspProArgLysHisPhe 453
229 CTGCGCGAAGCGCTGCGTGTGCTGCGGCGAGTGCCTGCGAGTGAAGAGACCCCTC 170
454 PheLysThrIleAspPheProArgLeuGluAlaGlyLeuIleGluProPheValPro 473
169 TTAAAGAGCTGAGCTTCAAGCGCGCTGAGAGTGGCAGTGTGAGCGCCCTTCAAGCT 110
474 AspProSerValValTyrAla 480
109 GACGTGAGTGCAGCCCATCTCC 89

RESULT 7

B0066445 968 bp mRNA linear EST 02-APR-2002
LOCUS AGENCOURT 6861074 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5931090
DEFINITION 5', mRNA sequence.

ACCESSION B0066445
VERSION B0066445.1 GI:19895491
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 968)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@p51-nih.gov

Tissue Procurement: Ion Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILML at:

http://image.llnl.gov

Plate: L16M2111 row: 2 column: 19

High quality sequence stop: 636.

Location/Qualifiers

1..968

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5931090"

/tissue_type="Lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH MGC 99"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GCCACGAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH_MGC

Library."

ORIGIN

Alignment Scores:

897 GAACTTAAATTT
|||||
||::||

296 TyrSerAlaGlnLeuAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
|||||.....|

Y 296

.....CGAGGAGGAGCGGGCCCTTGTTT 182

QY 316 AspMetLysProGluValLeuLeuAspAspLeuGlyAsnCySargLeuSerAspLeu 335
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 QY 336 GYLeuAlaValGluMetLysGlyGlyLeuProLethGlnArgAlaGlyThrAsnGly 355
 DB 303 GGCTTGCTGTGAAGATCCCGAGAGACCTGATCCGGCGCGGGGAGGACCTGTGGC 362
 QY 356 TTTMetAlaProGluLeuMetGluLysValSerTyrSerTyrProValAspTyrPhe 375
 DB 363 TACATGGCTCCAGAGGCTCTGAACAACAG---AGTACGGCGCTAGACCCGACTACTG 419
 QY 376 AlMetGlyCysSerLeuTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
 DB 420 GGCTTGCTGTGCTCATCTATGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
 QY 396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
 DB 480 GAGAAAGGTGAAGCGGAGAGAGAGTGAACCGCGGCTCTGAGAGAGAGAGAGTGTACTCC 539
 QY 416 HisAspAsnPheThrGluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysPro 435
 DB 540 CAC---AAGTTCTCCAGAGAGGCGCAAGTCCATCTGCAAGATGCTGCTCAAGAAAGATGCG 596
 QY 436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisAspPhe 454
 DB 597 AAGCAAGAGGCTGGGCTGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656
 QY 455 LysThrIleAsnPheProArgLeuGluGlnAlaGlyLeuIleGluProPheValProAsp 474
 DB 657 AGGAACATGAACTTCAAGCGCTTAGAGCCGGAGTTTGAACCTTCTCTGCTTCTGCAAC 716
 QY 475 ProSerValValTyrAlaLysAspLleAlaGluIleAspAspPheSerGluValArgLys 494
 DB 717 CCCCCGCTGTACTGTAAAGACGTGCTGACATGCAAGTTCTCACGTGAAAGGAGC 776
 QY 495 ValGluPheAspAspLysAspLysGlnPheLysAsnPheAlaThrGlyAlaValPro 514
 DB 777 GTCAATCTGACACACACACACACACACTTCTACTCAAGTCTCCACCGGCTGTGTCC 836
 QY 515 TLeuAlaTyrGlnGluGluIleLeuThrGlyLeuPheGluGluLeuAsn----- 531
 DB 837 ATCCCATGGCAAAACGATGATGATAAACAAGATCTTTTAAAGCTGAACGTGTTCG 896
 QY 532 -----AspProAsnAspPro 536
 DB 897 AACCTATGATACCTCCCGCCCA 921
 RESULT 9 1017 bp mRNA linear EST 02-APR-2002
 B0061150
 LOCUS AGENCOURT_6862973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
 DEFINITION 5', mRNA sequence.
 B0061150
 ACCESSION B0061150.1 GI:19848436
 VERSION
 KEYWORDS EST. Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1017)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>

Plate: LICK2083 row: h column: 07
 High quality sequence stop: 697.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5920182"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_99"
 /note="Organ: lymph. Vector: pOT7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Alignment Scores: 9,22e-72 Length: 1017
 Pred. No.: 813.50 Matches: 154
 Score: 71.72% Conservative: 59
 Percent Similarity: 51.85% Mismatches: 81
 Best Local Similarity: 28.16% Indels: 3
 Query Match: 13 Gaps: 3

DB: US-10-044-205A-2 (1-553) x B0061150 (1-1017)

QY 236 AlAlaLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAla 255
 DB 3 GCCCTCAATGAGAAACATCTCTGAGAGAGTCAACAGTGTGTGTGCTCAACTGGCC 62
 QY 256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAsp 275
 DB 63 TATGCTGACAGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 122
 QY 276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerLysValIlePhe 295
 DB 123 CTGAAGTTCACATCTACACATGAGGACCCCTGCTTGAAGAGAGAGGAGGAGGAGGAG 182
 QY 296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
 DB 183 TATGGGAGAGATCTCTGCGGCTTAGAAGACTTCCACCTGAGAAACCCGCTTACCGA 242
 QY 316 AspMetLysProGluValLeuLeuAspAspLeuGlyAsnCySargLeuSerAspLeu 335
 DB 243 GATCTGAACCTGAAACATCTCTGTAGATATATAGGCAATAGATCTAGACCTG 302
 QY 336 GYLeuAlaValGluMetLysGlyGlyLeuProLethGlnArgAlaGlyThrAsnGly 355
 DB 303 GGCTTGCTGTGAAGATCCCGAGAGACCTGATCCGGCGCGGGGAGGACCTGTGGC 362
 QY 356 TTTMetAlaProGluLeuMetGluLysValSerTyrSerTyrProValAspTyrPhe 375
 DB 363 TACATGGCTCCAGAGGCTCTGAACAACAG---AGTACGGCGCTAGACCCGACTACTG 419
 QY 376 AlMetGlyCysSerLeuTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
 DB 420 GGCTTGCTGTGCTCATCTATGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
 QY 396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
 DB 480 GAGAAAGGTGAAGCGGAGAGAGTGAACCGCGGCTCTGAGAGAGAGAGAGTGTACTCC 539
 QY 416 HisAspAsnPheThrGluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysPro 435
 DB 540 CAC---AAGTTCTCCAGAGAGGCGCAAGTCCATCTGCAAGATGCTGCTCAAGAAAGATGCG 596
 QY 436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisAspPhe 454

Db 597 AAGCAGAGGCTGGCTGAGAGGAGGCTGACAGAGCTCAAGACAGCCCTTTCTTC 656
 Qy 455 LysThrIleasnPhenProArgLeuGluAlaGlyLeuIleGluProPhoPheValProAsp 474
 Db 657 AGGAACATGACTTCAAGGCTTAGAAGCCGGAGTGTGACACCTCCCTTCCTTCAGAC 716
 Qy 475 ProSerValValIleValAlaAspIleAlaGluIleAspPheSerGluValArgly 494
 Db 717 CCCCCGCTGTGACTGACAGAGCTGAGAGCTGAGAGCTTCCTCAGTGGAAAGGC 776
 Qy 495 ValGluPheAspIleAspIleValAlaGlyLeuIleGluProPhoPheValPro 514
 Db 777 GTCAATCTGACACAGACAGAGCTTCTCAAGTTCTTCACGAGCTGTCTTC 836
 Qy 515 IleAlaTrpGlnGluGluIleIleGluTrpGlyLeuPheGluGluValAsn 531
 Db 837 ATCCCATGCAACAGAGATGATGAAACAGAACTTTTAAAGAGCTGAC 887

RESULT 10
 BQ061148 1019 bp mRNA linear EST 02-APR-2002
 LOCUS AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
 DEFINITION BQ061148
 VERSION BQ061148.1 GI:19894933
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NIH-MGC http://mgs.nci.nih.gov/
 1 (bases 1 to 1019)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 http://image.llnl.gov
 Plate: L10CM2083 row: h column: 05
 High quality sequence stop: 704.

FEATURES
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 Location/Qualifiers
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 /clone="IMAGE:5920180"
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 /lab_host="DH10B (phage-resistant)"
 /clone_idb="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB; Site_1: XhoI; Site_2:
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-CDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: This is a NIH_MGC
 Library."

ORIGIN

Alignment Scores:
 Pred. No.: 9.58e-71 Length: 1019
 Score: 803.50 Matches: 151
 Percent Similarity: 72.54% Conservative: 55
 Best Local Similarity: 53.17% Mismatches: 77
 Query Match: 27.81% Indels: 1
 DB: 13 Gaps: 1

US-10-044-205a-2 (1-553) x BQ061148 (1-1019)

Qy 157 PheLeuGlnGluGlnProPheIleAspPheValThrSerAlaPheTyrAspLeu 176
 Db 15 TACCTGAGCGTGGCCCTTTTGCAGTACCTCGACAGCATATCTTAAACGGTTCCG 74
 Qy 177 GlnTrpIleuPheGluMetGlnProValSerAspIleTyrPheTrpGluPheArgVal 196
 Db 75 CAGTGAAGTGGCTGGAAGAGCGACAGTGAACCAAAACACCTTCAGCAATCCAGTCC 134
 Qy 197 LeuGlyIleGlyIlePheGlyValValCysAlaValAlaGlnValIleValSerThrGlyIleMet 216
 Db 135 CTGGGCAAGAGTGGCTTTTGGAGAGTGGCTTCCAGAGTGGCGGCGGACAGGTAAGT 194
 Qy 217 TyrAlaCysIleIleValAspIleValArgLeuIleValIleGlyIleGlyIleMet 236
 Db 195 TATGCTTCAAGAGCTTGAAGAAAGAGGATGAGAAAGCGGAGGAGGAGGAGGAGGAG 254
 Qy 237 LeuLeuGluIleGluIleGluIleValValSerSerProPheIleValSerLeuAlaTyr 256
 Db 255 CTGAACGAGAGAGATCTCTGAGAGAGTGAACAGTGAAGTGAAGTGAAGTGAAGTGAAG 314
 Qy 257 AlaPheGluSerIleTyrHisIleCysValLeuValMetSerLeuMetLeuGlyIleAspLeu 276
 Db 315 GCTATGAGACCAAGAGAGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 374
 Qy 277 LysPheIleIleTyrAsnValGlyThrArgIleValAspMetSerArgValIlePheTyr 296
 Db 375 AAGTTTCACTTCAACATGAGATGGGCGAGGCTTCCCGAAGCGGCGGCTCTTCTAC 434
 Qy 297 SerIleAlaIleIleCysGlyMetLeuHisIleLeuIleGluIleValIleValTyrArgAsp 316
 Db 435 GCGGCGAGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 494
 Qy 317 MetIleProGluIleValLeuValAspLeuGlyIleValIleValIleValIleValIleVal 336
 Db 495 CTGAAGCCGAGACATCTTGTGATGACAGCGGACATCCGACATCTGACCTTGA 554
 Qy 337 LeuAlaValGluMetIleGlyIleValIleValIleValIleValIleValIleValIleVal 356
 Db 555 CTAGCTGTGATGCTCCGAGGCGGACAGACATCAAGGCGGTGTGGGACCGTGGTTAC 614
 Qy 357 MetAlaProGluIleLeuMetGlyIleValSerIleTyrProValAspTrpPheAla 376
 Db 615 ATGCTCCGAGAGTGTGAGAAATGA---CGGTACAGCTTACAGCCCTGAGTGTGGG 671
 Qy 377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheIleValIleValIleVal 396
 Db 672 CTGCGCTGCTCTCTGACGATGATCCAGGCGGCTGCTTCCACAGAGAGAG 731
 Qy 397 LysValSerIleValAspLeuIleValIleValIleValIleValIleValIleValIleVal 416
 Db 732 AAATTAAGCGGAGAGAGTGAAGGCTGCGGTGAAGAAATCCCGAAGATATTCG 791
 Qy 417 AspAsnPhenTrpGluGlnAlaIleValIleValIleValIleValIleValIleValIleVal 436
 Db 792 AGGCTTTTTCGCCGAGCGGCTCACTTGTCTCAAGCTCTCTGCAAGAGACCTTGC 851
 Qy 437 GlnArgLeuGly 440
 Db 852 GAACGCTGGG 863

RESULT 11
 BQ063841 1028 bp mRNA linear EST 02-APR-2002
 LOCUS AGENCOURT_6832078 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925495
 DEFINITION BQ063841
 VERSION BQ063841.1 GI:19891943
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

/clone.lib="NIH_MGC_101"
 /note="Organ: lung; Vector: pOMB7, site 1. EcoRI; Site 2:
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC library."

ALIGNMENT SCORES:

Score: 9,92e-70 Length: 934
 Percent Similarity: 71.93% Matches: 151
 Best Local Similarity: 52.98% Conservative: 54
 Query Match: 27.45% Mismatches: 78
 DB: 13 Indels: 2
 Gaps: 2

US-10-044-205a-2 (1-553) x B0526699 (1-934)

QY 157 PheLeuGlnGlnGlnProPhelysAspPheValThrSerAlaPheTyraAspPheLeu 176
 Db 78 TACCTGAGGAGGAGCAACATTCACGAATATCTGGACAGCATGTTTTGACCCGCTTCTC 137
 QY 177 GlnTrpLysLeuPheGlnMetGlnProValSerAspLysTyrrPheThrGluPheArgVal 196
 Db 138 CAGTGGAGATGGTTGGAAAGGCAACGGGTGACAAAACACCTTGAGCGATATCAGTG 197
 QY 197 LeuGlyLysGlyGlyPheGlyGlyValCysAlaValGlnValLysAsnThrGlyLysMet 216
 Db 198 CTAGAAAGGGGGGCTTCGGGAGAGTCTGCTGCTCCGACAGTTCGGGCGCAAGGTAAGG 257
 QY 217 TyraLysLysLysLeuAspLysLysArgLysLysLysGlyGlyGlyLysMetAla 236
 Db 258 TATGCTCGAAGCCCTTGAGAGAGAGAGATCAAAAAGAGAGAGAGGAGTCCATGCGC 317
 QY 237 LeuLeuGlnLysGlnLysLeuGlnLysValSerSerProPheLeuAlaSerLeuAlaTy 256
 Db 318 CTCATAGGAAGAGATCTCTCAAGAGGTCAACAGTCACTTGTGTCACCTGCGCTAT 377
 QY 257 AlaPheGlnSerLysThrLysLeuCysLeuValMetSerLeuMetAsnGlyGlyLysLeu 276
 Db 378 GCTACGAGACCAAGAGATGCACTGCTGCTGCTCTCAACATCAAGATGAGGATCCTG 437
 QY 277 LysPheHisLysLysValGlyThrArgGlyLeuAspMetSerArgValIlePheTy 296
 Db 438 AAGTTCACATCTACAAACATGCGCAACCTGCTCGAGAGAGAGGCGGCTTGTATT 497
 QY 297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyraArg 316
 Db 498 GCGGAGAGATCTCTGCGGCTTGAAGACCTTCCACCGTGAACAACCGCTTACCGAGAT 557
 QY 317 MetLysProGlnLysValLeuAspPheLeuGlyLysCysArgLeuSerAspLysGly 336
 Db 558 CTGAAACCTGAACATCTCTGTAGATGATTTAGGCCACATTTAGATCTCAACCTGAGC 617
 QY 337 LeuAlaValGlnMetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTy 356
 Db 618 TTGGCTGTGAAGATCCCGAGGAGAGCTGATCCCGGCGGAGGAGCACTGTTGGCTAC 677
 QY 357 MetAlaProGlnIleLeuMetGlnLysValSerLysTyrrProValAspTrpPheAla 376
 Db 678 ATGGCTTCAGAGAGTCTGAAACCAAG--AGGTACGCGCTGAGCCCGACCTACTCGGAGC 734
 QY 377 MetGlyCysSerLysLysGlnMetValAlaGlyArgThrProPheLysAspTyLysGln 396
 Db 735 CTGGCTGCTCATCTATAGAGATGATGAAAGCCAGTCCGCTTCCGCGAGCAAGAGAG 794
 QY 397 LysAlaSerLysGlnAspLysLysGlnArgThrLeuGlnAspGlnValLysPheGlnHis 416
 Db 795 AAGGTGAAGCGGAGAGAGAGTGAACCGCGCGTCTCTGAGAGCGGAGAGAGATGATCC 854

QY 417 AspAspPheThrGlnGlnLysAlaLysAspLysArgLysLeuPheLeuAlaLysLys--Pro 435
 Db 855 ACAAGTTCTCCAGAGAGAGGAGGATCCATCTCGAAGATGCTGCTCAAGAAAATGCCNA 914
 QY 436 GlnGlnArgLeuGly 440
 Db 915 ANCAAAAGCTGGGC 929

RESULT 13

B0057469

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..1058

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="NIH_MGC_99"

/note="Organ: lymph; Vector: pOMB7, site 1: XhoI; site 2:
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

ALIGNMENT SCORES:

Pred. No.: 1,18e-69 Length: 1058
 Score: 793.00 Matches: 157
 Percent Similarity: 69.93% Conservative: 59
 Best Local Similarity: 50.81% Mismatches: 85
 Query Match: 27.45% Indels: 9
 DB: 13 Gaps: 2

US-10-044-205a-2 (1-553) x B0057469 (1-1058)

QY 157 PheLeuGlnGlnGlnProPhelysAspPheValThrSerAlaPheTyraAspPheLeu 176
 Db 15 TACCTGAGGAGGAGCCCTTTTCCGATCTACGACAGATCTTCAACCGTTCCTG 74
 QY 177 GlnTrpLysLeuPheGlnMetGlnProValSerAspLysTyrrPheThrGluPheArgVal 196
 Db 75 CAGTGGAGATGGTTGGAAAGGCAACGATGACAAAACACCTTGAGCGAGATACCGAGTC 134

197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
 135 CTGGGCAAGAGTGGCTTTGGGAGAGTGTGGCTCTCCAGGTGGGCGCACAGTAAATG 194
 217 TTTAACTGlyLysLeuAspLysLysLysLysLysLysLysLysLysLysLysLysLys 236
 195 TATGCTGCAAGAGTGGTAAAGAAAGGAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAG 254
 237 LeuLeuGlyLysGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 256
 255 CTGAACAGAGAGAGTCTGAGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 314
 257 AlaPheGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 276
 315 GCTATGAG 374
 277 LysPheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 296
 375 AAGTTCACATCTACACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434
 297 SerAlaGlnIleAlaCysGlyMetLeuHisLysLysLysLysLysLysLysLysLys 316
 435 GCGCGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
 317 MetLysProGluAsnValLeuLeuAspLysLysLysLysLysLysLysLysLysLys 336
 495 CTGAAGCCGAG 554
 337 LeuAlaValGlyMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 356
 555 CTAGCTGTGATGAG 614
 357 MetAlaProGluIleLeuMetGlyLysLysLysLysLysLysLysLysLysLysLys 376
 615 ATGGCTCCGAG 671
 377 MetGlyCysSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 396
 672 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
 397 LysValSerLysGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 416
 732 AAGATCAAGCGGGG-ACGAGGTGAGCCCGCTGGTAAAGAGAGAGAGAGAGAGAGAG 790
 417 AspAsnPheThrGluGlnAlaLysAspLysCys-ArgLeuPheLeuAlaLysLysPro 436
 791 AGCGCTTTTCCCGAGGCGCCGCTCACTTGTCTCAAGCTTCTCTGCAAGAGAGAGAG 850
 436 uGlnArgLeuGlySerArgLysLysLysLysLysLysLysLysLysLysLysLysLys 450
 851 CGAGCGCTGGGGGGGGGTTCCGGGGGGGCAACCGGCCCCCAAGGTTGAAGAGAGAGAG 910
 451 -HisLysPhePheLysThrLysLeu 458
 911 CCTCTCTTTTAAAGAGTAAAC 935

RESULT 14
 EX392018/c 917 bp mRNA linear EST 13-MAY-2003
 LOCUS EX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0D1010YD11 3-PRIME, mRNA sequence.
 ACCESSION EX392018
 VERSION EX392018.1 GI:30607809
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 917)
 AUTHORS Li W.B., Gruber C., Jesse J., and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

FEATURES

source

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f for
 more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BA1046ZH12_CS04416_1&cluster=3090.f
 Contact : Feng Liang Email : fliang@life.techn.com URL :
<http://fulllength.invitrogen.com/Invitrogen/Corporation/1600>
 Faraday Avenue Genoscope sequence ID : CS0BA1046ZH12_CS04416_1.

Location/Qualifiers

1..917
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 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /clone_id="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1,37e-69 Length: 917
 Score: 791.50 Matches: 149
 Percent Similarity: 72.82% Conservative: 60
 Best Local Similarity: 51.92% Mismatches: 71
 Query Match: 27,40% Indels: 7
 DB: 13 Gaps: 3

US-10-044-205A-2 (1-553) x EX392018 (1-917)

122 ProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaIleThrGlu--- 140
 891 CCTGATCCCTAAGTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 832
 141 -----GlnLysArgValAlaIleValThrLeuArgLysAlaGlnAlaMetAlaPheLeu 158
 831 CCTGCAAAAGACTTTTTCAGAACTACCCCGGCTGACCAAGAG-----TACTCG 781
 159 GlnGlnGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnThr 178
 780 ACGTGGCCCTTTTCCGAGCTACCTGACAGAGATCTTCAACCGTTTCTGCAAGTGG 721
 179 LysLeuPheGlnMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
 720 AAGTGTGAGAAAG 661
 199 LysGlyGlyPheGlyGlyValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
 660 AAGGTGGCTTTGGGAGAGGTGGCTGCGAGGTCCGGGCCACAGGTAAGATGATGCC 601
 219 CysLysLysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeu 238
 600 TCGAAGAGCTAGAGAAAG 541
 239 GlnLysGlnLysLeuGlyLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe 258
 540 GAGAGACAGATCTCGAGAAAGTGAACGTGGTTGTGATGAGCTTGGCTTACGCTAT 481
 259 GluSerLysThrHisLysCysLeuValMetSerLeuMetAsnGlyLysAspLysPhe 278
 480 GAGAGCCAG 421
 279 HisLysLysValGlyThrArgLysLysLysLysLysLysLysLysLysLysLysLys 298
 420 CAGTCTTCAATAGAGGAG 361

Db 683 GTGATAAAGATGAA---CGCTACACTTTTACCCCGACTGTGGGTTTGCTCTC 739
 QY 381 ILLETyGluMetVal-ALAGIYArgThrProPheLysAspTyrLysGluysValSerIy 400
 Db 740 ATTATGAGATGATTCGAAGGCCCATCTTCCTTCGCGACGGGMAAGAACGATTAATAA 799
 QY 400 s---GluaspLeuLysGlnArg 406
 Db 800 GGGAAAGAGGTTGAAAAAAGG 821

Search completed: August 13, 2004, 21:10:27
 Job time : 2727 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: August 13, 2004, 18:45:41 ; Search time 92 Seconds

(without alignments)
3335.737 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2889

Sequence: 1 MYDMGALNLTANTAYLQAR.....NRPTGEBNSKSVCLLL 553

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents NA -OPMT=fastac -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOBCU=0
-LOOPEXT=0 -INITTS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

1: Issued_Patents NA:*
2: /cgnt2_6/prodata/2/ina/5A.COMB.seg:*
3: /cgnt2_6/prodata/2/ina/5B.COMB.seg:*
4: /cgnt2_6/prodata/2/ina/6A.COMB.seg:*
5: /cgnt2_6/prodata/2/ina/6B.COMB.seg:*
6: /cgnt2_6/prodata/2/ina/6C.COMB.seg:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2883	99.8	1662	4	US-09-802-117-1
2	2883	99.8	2249	4	US-09-802-117-5
3	2876	99.6	1662	4	US-09-738-894A-1
4	2876	99.6	1662	4	US-09-738-894A-1
5	1801	62.3	1062	4	US-09-964-469-1
6	1528	52.9	36651	4	US-09-802-117-3
7	1528	52.9	36651	4	US-09-738-894A-3
8	1280.5	44.3	2113	4	US-09-964-469-3
9	1252.5	43.4	2511	4	US-09-614-748A-7
10	1252.5	43.4	2529	4	US-09-417-197-60
11	1252.5	43.4	2529	4	US-09-417-197-42
12	1250.5	43.3	1975	4	US-09-016-434-1298
					Sequence 9, Appli

13	1243.5	43.0	2017	4	US-09-614-748A-8	Sequence 8, Appli
14	1240	42.9	2848	3	US-08-464-954A-2	Sequence 2, Appli
15	1238	42.9	2204	1	US-08-221-817-12	Sequence 12, Appli
16	1238	42.9	2204	1	US-08-454-439-12	Sequence 12, Appli
17	1238	42.9	2204	5	PCT-US94-10487-12	Sequence 12, Appli
18	1236.5	42.8	2204	5	US-08-464-954A-1	Sequence 12, Appli
19	1210.5	41.9	1879	4	US-09-614-748A-10	Sequence 10, Appli
20	1210.5	41.9	1879	4	US-07-980-526-1	Sequence 10, Appli
21	1209.5	41.9	2206	1	US-08-221-817-10	Sequence 10, Appli
22	1209.5	41.9	2206	1	US-08-454-439-10	Sequence 10, Appli
23	1209.5	41.9	2206	5	PCT-US94-10487-10	Sequence 10, Appli
24	1189	41.2	1983	1	US-08-221-817-21	Sequence 21, Appli
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26	1189	41.2	1983	5	PCT-US94-10487-21	Sequence 21, Appli
27	1023.5	35.4	1420	4	US-09-614-748A-11	Sequence 11, Appli
28	981.5	34.3	1305	4	US-09-614-748A-12	Sequence 12, Appli
29	725.5	25.1	2362	4	US-09-620-312D-273	Sequence 12, Appli
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31	507	17.5	3255	4	US-09-016-434-1471	Sequence 1306, Ap
32	493	17.1	2754	3	US-09-429-322-3	Sequence 1471, Ap
33	473.5	16.4	2274	4	US-09-772-647-3	Sequence 3, Appli
34	469	16.2	2104	4	US-09-313-930-1	Sequence 3, Appli
35	469	16.2	2104	3	US-09-023-655-1191	Sequence 1191, Ap
36	469	16.2	2549	3	US-09-467-082-3	Sequence 3, Appli
37	469	16.2	2549	4	US-09-394-455-5	Sequence 5, Appli
38	466.5	16.1	1599	4	US-09-256-465-1	Sequence 1, Appli
39	466.5	16.1	1599	4	US-09-167-322-3	Sequence 3, Appli
40	466.5	16.1	1599	4	US-09-023-655-1004	Sequence 1004, Ap
41	465	16.1	1788	4	US-09-417-197-68	Sequence 68, Appli
42	461	16.0	2181	4	US-09-417-197-70	Sequence 70, Appli
43	459	15.9	2968	4	US-08-685-852-1	Sequence 1, Appli
44	458.5	15.9	2610	2	US-09-212-771-1	Sequence 1, Appli
45	458.5	15.9	2610	3	US-09-091-058-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-802-117-1
Sequence 1, Application US/09802117
Patent No. 6444456
GENERAL INFORMATION:
APPLICANT: Walke, D. Made
APPLICANT: Wiganowski, Nathaniel L.
TITLE OF INVENTION: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymers
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/09/802,117
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/188,449
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1662
TYPE: DNA
ORGANISM: homo sapiens
US-09-802-117-1

Alignment Scores:

Pred. No.: 0
Score: 2883.00
Percent Similarity: 99.82%
Best Local Similarity: 99.82%
Query Match: 99.79%
DB: 4
Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662)

QY 1 MetValaSpMetGlyAlaLeuAspAsnLeuIeAlaAsnThrIaTYrLeuGlnIaIaArg 20
DB 1 ATGGTGGACATGGGGGCGCTGGAGVAACTGATGCCACACCGGCTGACGGCGCGG 60

QY 21 LysProSerAspCyAspSerIysGlyLeuGlnIleArgIleArgIleSerLeuAlaLeuPro 40
 Db 61 AAGCCCTCGACTGCGACGGAAAGAGCTCGACGGCGCGCGCTGAAGCTCGCGCTGGCC 120
 QY 41 GlyLeuGlnGlyCyAsnIleGluLeuArgIleLeuSerLeuAsnPhenIleSerLeuCyS 60
 Db 121 GGGCTGGAGGGCGCGCGGAGCTTCGCCGAAAGCTGTCCTCGTAACCTTCGACAGCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGCAGGCCCATGGGTGCGCGCTTCCTTCGTCGACTTCCTAACCAAGTCCACGTTTC 240
 QY 81 ArgIysAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
 Db 241 GCGAAGCGCGCAACCTTCCTGAGAGAGCGGACGAGAACTGGAGAGCTGGCGAGAGAGACC 300
 QY 101 ThrIysAspSerAlaLeuGlnGlyLeuValAlaThrCyAsnIleSerIleProAlaProGly 120
 Db 301 ACCAAAGACGCGCGCTGAGGGCGCTGGGGCACTGTGTGAGTCCCGCTCCCGCGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrIysCySglnAlaIleThrGln 140
 Db 361 AACCGCAACCTTCCTCGACCAAGCCGTGGCCACAGAGTCCAGACACCACTGAG 420
 QY 141 GluGluArgValAlaIleValThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGln 160
 Db 421 GAAAGCGAGGCTGCTCACTGACGACGCTGGCCGCGCTGGCGGCAATGCTTCCTCGAAG 480
 QY 161 GlnProPheIysAspPheAlaThrSerIlePheIysTrpAspIysPheLeuGlnTrpLeu 180
 Db 481 CAGCCCTTAAAGATTGCTGTGACAGAGCCCTTCAGACAAATTTCGAGAGGAAATC 540
 QY 181 PheGluMetGlnProValSerAspIysTyrPheThrGlnPheArgValLeuGlyIysGly 200
 Db 541 TTCGAGAGCAACCGATGTCAGACAAAGTCTCACTGAGTTCAAGAGTCTGGGAAAGGT 600
 QY 201 GlyPheGlyGlyValCyAsnAlaValGlnValIysAsnThrGlyIysMetCysIleCysIys 220
 Db 601 GGTTTGGGAGGTATGTGCTCGTCAGAGTAAACACTGGAGAGATGATGCTCTGAG 660
 QY 221 LysLeuAspIlyIysArgLeuIysIleIysGlyGlyIysMetAlaLeuLeuGlnIys 240
 Db 661 AAACCTGACAAAGCCGCTGAGAAAGAAAGGTGGAGAAAGATGCTCTCTTGGAAAG 720
 QY 241 GluIleLeuGlnIysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAATCTTGAGAAAGTCAAGACCCCTTCATGTCTCTCTGGCCCTTATGAGAGC 780
 QY 261 LysThrIleAsnCySleuValMetSerLeuMetAsnGlyGlyAspLeuIysPheIle 280
 Db 781 AAGACCCATCTGCTCTTGTCATGAGCCTGATGAAGGGGAGAGCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgIysLeuAspMetSerArgValIlePheIysSerAlaGlnIle 300
 Db 841 TACAACTGGGACGCTGCGCTGACATGAGCGCGGTATCTTTCATCGGCCCAATA 900
 QY 301 AlaCysGlyMetLeuIleIleuIleGluLeuGlyIleValTyrArgAspMetIysProGln 320
 Db 901 GCGTGGGGATGTGCACTCCATGAATCTCGGCACTGCTCATCGGACAGAGAGCCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCyArgLeuSerAspLeuGlyLeuAlaValGln 340
 Db 961 AATGTGCTCTGAGATGACCTCGCAACTGCACTGAGTTATCTGACCTGGGCGCTGGAG 1020
 QY 341 MetIysGlyIysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGln 360
 Db 1021 ATGAAAGGTGGCAACCCATCCACAGAGGCTGAAACAAATGTTATATGGCTCTGAG 1080
 QY 361 IleLeuMetGlyIysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCTATATGGAAGAAAGTATAGTATCTCTATCTCTGTGACATGGTTGGCATGGATGACAC 1140

Qy	381	ILEYRGIUNETVALNAGLYATGTRProheliysASDLYLysGILysVALSerIys	400
Db	1141	ATTATGTGAAATGGCTCTCGAGCAAGAACCATTCGAAAGATTACAGAGAAAGGTGAGTAA	1200
Qy	401	GIUAspLeuLYSGInRThLeuGInAspGInVALIysPheGInhiSAAsPAspHeThr	420
Db	1201	GAGGATCTGAGCGAAGAACCTCTGCAGAACAGAGTCAAAATTCGACGATGATACCTTCACA	1260
Qy	421	GIUGInuAlaIysAsp11eCyArGLeuPheLeuAlaIysIysPProGIUGInArGLeuGInI	440
Db	1261	GAGAGAGCAAAAGATTGTCGAGGCTCTCTTGGCTGTAGAAACGAGAACGCTTAGGA	1320
Qy	441	SeArGILysSerSerAspAspProArGILysIshIspPheIysThr11eAsnPhePro	460
Db	1321	AGCAGAGAAAGTCTGATGATCCAGAGAAACATCAATTCCTTTAAACATCAACTTCTCT	1380
Qy	461	ArGLeuGInuAlaGIysLeu11eGIuProPheValProAspProSeValValTYraLa	480
Db	1381	CGCCTGAGAGGCTGACCTTAATTGAACCCCATTTGTGGCAACCCCTTCAGTGGTTATGCC	1440
Qy	481	LYAsp11eAlaGInu11eAspAspPheSerGIuVALArgGIyVALGIuPheAspAspIys	500
Db	1441	AAGAGCATGCGTGAATAATGATGATTTCTCGAGGTTGCGGAGGTGAATTGAAGACAA	1500
Qy	501	AspIysGInPhePheIysAsnPha11eThrGIyALaVALPro11eAlaTrpGInGIuGIn	520
Db	1501	GATACAGCAATCTTCACAAAACTTGGCAGACGGGCTGTCTCTATACATGCGAGAGAGAA	1560
Qy	521	11e11eGIuThrGIyLeuPheGIuGIu11eAsnAspProAsnArPProThrGIyCySGIn	540
Db	1561	ATTATGAGAAACGGACCTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGTGAG	1620
Qy	541	GIuGIyAsnSerSerIysSerGIyVALCyALeLeuLeu	553
Db	1621	GAGGTAATTATCCAAAGTGTGGCGTGTGTTTATATG	1659

RESULT 2

US-09-802-117-5
: Sequence 5, Application US/09802117

Patent No. 6444456

APPLICANT: Walke, D. Wade

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. 6444456e1 Humman
; TITLE OF INVENTION: Encoding the Same
: TITLE OF INVENTION: Encoding the Same

FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/09/802,117

CURRENT FILING DATE: 2001-03-08
CURRENT FILING NUMBER: IIS 60/188.449

PRIOR FILING DATE: 2000-03-10

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; NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0

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: SEQ ID NO 5
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: LENGTH: 2249

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TYPE: DNA

US-09-802-117-5

Alignment Scores:

Pred. No.:	0	Leng
Score:	2883.00	Match

Percent Similarity:	99.82%	Cons
Percent Similarity:	99.82%	Mism

Best Local Similarity:	99.02%	Index
Query Match:	99.79%	Case

DB: 4 08/23

US-10-044-205A-2 (1-553) X US-09-802-117-5

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 DB 121 GGGCTGACAGGGCTGCGCGAGCTCGCCAGAACTGCTCCGAACTTCCACAGCTGCTGCT 180
 QY 61 GluGlnGlnProIleGlyArgGluPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCCATCGCTGCGCTCTTCGTAATCTTCAGCCAGCAGGCGCCACGCTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
 DB 241 CCGAAGCGCGCACTTCTTCAAGGACCTGCAAACTGGAGAGCTGGCGCGAGGAGGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAAGACACCGCGCTGACAGGGGCTGCTGCGCACTTGCGCAGAGCCCTGCGCGAG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCGCAACCTTCTTCACGACGCGCTGGCCACCAATGCGCAAGCGCACCACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAGGCGAGTGGCTGACGAGCGCTGGCCAAAGCTGAGGCGCATGCTTCTTGGCAAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTrpAspLysPheLeuGlnTrpLysLeu 180
 DB 481 CAGCCCTTTAAGGATTCGTGACAGCGCTTCTTACCAAGATTCGCAAGTGAAGCTC 540
 QY 181 PheGluMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlnLysGly 200
 DB 541 TTGAGATGCAACCGATGTCACAGACGATCTTCACTGAGTTCAGAGTCTGGGGAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnAlaLysAsnThrGlyLysMetTrpAlaCysLys 220
 DB 601 GCTTTGGGAGGATATGCGCTCCAGGTGAAGAACTGGGAAAGATGATGCTGCTGAAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlnLysMetAlaLeuLeuGlnLys 240
 DB 661 AAATGACAAAGAGCGCTGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGluSer 260
 DB 721 GAATCTCTGAGAAAGGATGAGGAGCTTCACTGATGCTCTGCGCTGAGGAGCTTGAAG 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLysPheHisIle 280
 DB 781 AAGGCCATCTGCTGCTGCTGATGAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
 DB 841 TACAACTGCGGACCGCGTGGCTGACATGAGCGCGGATCTTTTACTCGGCCAATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 DB 901 GCTGTGAGATGCTGACCTCACTGAACTCGGCACTCGCTATGAGGACATGAAAGCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 DB 961 AATGTCTTCTGAGTACCTCGCACTGCAAGGATGATCTGACCTGGGCGCTGGCGT 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTrpMetAlaProGlu 360
 DB 1021 ATGAAGGGGTGGCAAGCCATCAACCAAGGGGCTGAAACCAATGGGTACATGCTCTGAG 1080
 QY 361 IleLeuMetGlnLysValSerTrpSerTrpProValAspTrpPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGAGAAAGATTAATTTCTATCTGCTGAGCTGTTGCAATGGGAGGAGC 1140
 QY 381 IleTrpGluMetValAlaGlyArgThrProPheLysAspTrpLysGlyLysValSerLys 400
 DB 1141 ATTATGAAATGGTCTCTGAGAACCACTCAAAAGATTAACAGGAAAGGATGAGTAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAGAACTTGCAGACGAGGTCAAAATTCACATGATTAATTCA 1260
 QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnAlaGluGly 440
 DB 1261 GAGGAAGCAAAAGATTTGCAAGGCTCTTCTGCTAAGAAACAGCAAGCAAGCTTAGA 1320
 QY 441 SerArgGluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPro 460
 DB 1321 AGCAGAGAAATCTGATGATGATCCAGAAACATCATTTCTTAAACGATCACTTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
 DB 1381 CGCTGGAAAGCTGGCTTAATTAAGCCCATTTGTCACAGCTTCACTGATGATGCT 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500
 DB 1441 AAAGACATGCTGAAATTAATGATATTTCTGAGGTTGCGGGGCTGGAATTTGAGCA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 DB 1501 GATAGCAGTCTTCAAAATCTTGCAGAGGCTGCTCTTATACATGCGCAGAGAA 1560
 QY 521 IleIleGlnThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 DB 1561 ATTATGAAACGGGACTGTTGAGAGAACTGAATGACCCCAACGACTTACGGGTTGAG 1620
 QY 541 GluLysAspSerSerLysSerGlyValCysLeuLeu 553
 DB 1621 GAGGATTAATCATCAAGTCTGGGTGTGTGTATTG 1659

RESULT 4
 US-09-964-469-1
 ; Sequence 1, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: C0000636DIY
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-964-469-1

Alignment Scores:
 Pred. No.: 0 Length: 1662
 Score: 2876.00 Matches: 551
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 2
 Query Match: 99.55% Indels: 0
 DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

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 DB 1 ATGTGAGCAATGGGAGGCTCTGAGCAACTGATGCGCAACCGCTTACTGAGGCGCG 60
 QY 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCTTGGAGCTGCGACAGCAAGAGGCTGCAAGCGGCGGCGGAGTACCTGCGCTGCCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAspPheHisSerLeuCys 60
 DB 121 GGGCTGGAGGGGTGGCCGGAGCTCCGCCAGAAAGCTGCTCCGACCTTCCACAGCCCTGGT 180
 QY 61 GluGlnGlnProTlLeuArgLeuPheAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGGAGAGAGCCCATCGGTGGCCGCTCTTCCTCGAGCTTCCTAGCCACATGCGCCACGTTT 240
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGlnGluPro 100
 DB 241 CGCAAGGCGGCAACCTCTTAGAGAGAGTGCAGAACTGGAGAGCTGGCCGAGAGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAGACAGCGCCCTCCAGAGGCTGGTGGCCACTGTGGAGTGGCCCTGGCCCGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCCGCAACCTTCTCAGCCAGCGCCGTCAGCAAGGCGCAAGGCGCAACCACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAGAGCGAGTGGCTGGAGTGCAGCTGGCCAGAGCTGAGGCCATGGCTTCTTTCAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTrpAspLysPheLeuGlnTrpLysLeu 180
 DB 481 CAGCCCTTAAAGATTCCTGAGCAAGCCGCTTTCAGCAAGATTTCTGCGAGTGAACCTC 540
 QY 181 PheGluMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlyLysGly 200
 DB 541 TTCAGAGTGCACCAAGTGTGCAGCAAGTACTTCAGAGTTCAGAGTCTGGGAAAGGT 600
 QY 201 GlyPheGlnGluValCysAlaValGlnValLysAsnThrGlyLysMetTrpAlaCysLys 220
 DB 601 GGTGTTGGAGGATATGTGCTCCAGGTGAAAACACGAGGAGATGATGCTGTAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGluLysMetAlaLeuLeuGluLys 240
 DB 661 AAAGTGCAGCAAGAGCGGTGAGAAAGAAAGCTGGCGAAGATGGCTCTTCTTGGAAAAG 720
 QY 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGluSer 260
 DB 721 GAATCTTGGAGAGGTGCAGAGCCCTTCTTCTGCTCTGCTGCTTTCAGAGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
 DB 781 AAGACCCATCTCTGCTGTCTGATGAGCTGATGATGAGGAGGAGCACTCAAGTTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
 DB 841 TACAACGTGGGCAAGCGTGGCTGGACATGACCGGGGTGATCTTTTACCTGGCCCAAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
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 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGlu 340
 DB 961 AATGTGCTTCTGATGATCCTGCGCACTGAGAGTATCTGACCTGGGCGTGGCGTGGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTrpMetAlaProGlu 360
 DB 1021 ATGAAGGGGTGGCAAGCCCATCAACCAAGGCGCTGGAAACATGATGATGCTTCCAGAG 1080
 QY 361 IleLeuMetGlnLysValSerTrpSerTrpProValAspTrpPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGGGAAAGGTATATCTCTATCTGTGGAGCTGTTTCCATGGAGTGCAGC 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTrpLysGlnLysValSerLys 400
 DB 1141 ATTATGAAATGTTGCTGGAGCAACCACTTCAAGATTAACAAGGAAAGGTGACGTAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGGAAGCAAGAACTCTGCAGAGAGAGTGAATTCAGCAATGAACTTCA 1260
 QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 DB 1261 GAGGAGCAAAAGATATTGACAGCTCTTCTTGGCTAAGAAACAGAGCAAGCCTTAGGA 1320
 QY 441 SerArgGlyLysSerAspAspProArgLysHisPhePheLysTrpIleAsnPhePro 460
 DB 1321 AGCAGAGAAAGTCTGATATGATCCAGAAACATCATTTCTTAAAGATCAACTTCT 1380
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValIleTyrAla 480
 DB 1381 CGCTCGAAGCTGCTCAATTTGAACCCCACTTGGCCAGACCTTCAAGGTATATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 DB 1441 AAGACATCCCTGAATTTGATGATTTCTGAGAGTTCCGGGGGTGAAATTTATGACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 DB 1501 GATTAAGAGTTTCTCAAAAACCTTGCAGACAGTGGCTTCTTATAGCATGGAGAAATA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProLeuArgProThrGlyCysGlu 540
 DB 1561 ATTATAGAAAGCGAGACTTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTTGAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 DB 1621 GAGGATTAATTCACCAAGTCTGGGAGTGTCTTGTATTG 1659

RESULT 5

US-09-802-117-3
 : Sequence 3, Application US/09802117
 : Patent No. 6444456
 : GENERAL INFORMATION:
 : APPLICANT: Walke, D. Made
 : APPLICANT: Miganowski, Nathaniel L.
 : APPLICANT: Turner, C. Alexander Jr.
 : TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymic
 : FILE REFERENCE: LEX-0147-USA
 : CURRENT APPLICATION NUMBER: US/09/802,117
 : PRIOR FILING DATE: 2001-03-08
 : PRIOR APPLICATION NUMBER: US 60/188,449
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 1062
 : TYPE: DNA
 : ORGANISM: homo sapiens
 : US-09-802-117-3

Alignment Scores:

Pred. No.: 3,77e-202 Length: 1062
 Score: 1801.00 Matches: 349
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 62.34% Indels: 0
 DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-3 (1-1062)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGCTGACATGGGGGCTCTGACACCTGATGCGCAACCGCTTACCTGACAGGCCGG 60
 QY 22 LysProSerAspCysAspSerLysGlnLeuGlnArgGatGatGatGatGatGatGatGat 40
 DB 61 AAGCCCTGGAGTGCAGACGCAAGAAAGCTTCCAGCGGCGGCGGTGAGCTGGCCCTGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60

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Db      |||||
121  GGCGCTGCAAGGCGGAGCTCCGCGAAGCGTCTCGAATCTCCAGCCTGTGT 180
Qy      |||||
61  GGUUUGUINPRLLEGLYARIGRLEUPHEARGASPHELEUALATHRVAlProThr-Phe 80
Db      |||||
181  GAGCGAGCGACCGCTGCGGCTCTTCCTCGTGAATCTTCAGACAGAGGCCACGCTC 240
Qy      |||||
81  ARGYSALAAATHRPHLEUGLUASPVAlGlnAsnTPGluLeuAlaGluUuGlyPro 100
Db      |||||
241  CGCAAGGCGCAACCTTCCTAGAGGAGCGTGAAGACTGGGAGCTGGCGGAGAGGAGACC 300
Qy      |||||
101  THRYSASPSEALALEUGINGLYLEUVALAlaThrCysAlaSerAlaProAlaProGly 120
Db      |||||
301  ACCAAGACAGCGCGCTGCAAGGCGTGTGTGCACTTGAGAGTGGCCCTGCGCGG 360
Qy      |||||
121  AAsnProGlnProPheLeuSerGlnAlaValAlaThrCysCysGlnAlaAlaThrThrglu 140
Db      |||||
361  AACCGGCAACCTTCCTAGAGGAGCGTGTGCGCAAGGCTGCGCAAGGCGCAAGCTGAG 420
Qy      |||||
141  GUUGUARGVALAlaAlaValThrLeuArgValaGluAlaMetAlaPheLeuGlnUu 160
Db      |||||
421  GAAGAGCGAGTGGCTGAGTGAACGCTGGCGCAAGCTGAGGCGCAAGCTTCCTTGCAAGAG 480
Qy      |||||
161  GlnProPheLeuSAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
Db      |||||
481  CAGCCCTTTAAGATTTCGACACGCGCTTCCTAGACAGATTTCTGCGAGTGGAAACTC 540
Qy      |||||
181  PHEGLUMETGlnProValSerAspLysTrpPheThrGluPheArgValaLeuGlyLysGly 200
Db      |||||
541  TTGGAGATGCAACAGTGTGCAAGAGTCACTTCACTGAGTGTGAGAGTCTGGGAAAGGT 600
Qy      |||||
201  GLYPHEGLINGLYCYALAVAlGlnValLysAsnThrGlyLysMetTrpAlaCysLys 220
Db      |||||
601  GGTITTTGGGAGGATGTGCGCTCCAGGTGAAAACACTGGGAAAGTATGCTGTAAAG 660
Qy      |||||
221  LysLeuAspLysLysArgLeuLysLysLysGlyValGluLysMetAlaLeuLeuGluLys 240
Db      |||||
661  AAACCTGCAAGAAAGCGCTGAAAGAAAGGTGCGAGAGAGTGGCTCTTGGAAAG 720
Qy      |||||
241  GlnUleLeuGlnLysValSerSerProPheLeuValSerLeuAlaTrpAlaPheGlnSer 260
Db      |||||
721  GAAATCTGAGAAAGTACAGACCTTTCAATGTCTCTGGCCGATAGCTTGTAGAGAC 780
Qy      |||||
261  LysThrHisLeuCyLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
Db      |||||
781  AAGACCAATCTGTGCTTGTCAATGACCTGATGAATGAGGAGACCTCAAGTTCAATC 840
Qy      |||||
281  TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
Db      |||||
841  TACAACTGGGAGCGCGTGGCTGACATGAGCGGAGTACTTTTACTCGGCGGAGAT 900
Qy      |||||
301  ALAcysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGln 320
Db      |||||
901  GCCGTGGAGTGTGCTCACTTCATGAATCTGGCAATCGCTTATCGGAGCATGAACCTGAG 960
Qy      |||||
321  AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db      |||||
961  AATGTCTTGTGATGACCTCGCACTGAGAGTTATCTGACCTGGGAGCTGGCGTGGAG 1020
Qy      |||||
341  MetLysGlyLysLysProIleThrGlnArg 350
Db      |||||
1021  ATGAAGGAGTGGCAAGCCCATCAACCCAGAG 1050

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RESULT 6

US-09-738-894A-3

Sequence 3, Application US/09738894A

Patent No. 631423

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: C1000636

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CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651
TYPE: DNA
ORGANISM: Human
FEATURES:
NAME/KEY: misc feature
LOCATION: (1)..(36651)
OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

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Alignment Scores:

Pred. No.:	1,77e-167	Length:	36651
Score:	1528.00	Matches:	349
Percent Similarity:	41.40%	Conservative:	0
Best Local Similarity:	41.40%	Mismatches:	1
Query Match:	52.89%	Indels:	493
DB:	4	Gaps:	1

US-10-044-205A-2 (1-553) x US-09-738-894A-3 (1-36651)

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Qy      |||||
1  MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaThrLeuGlnAlaArg 20
Db      |||||
2076  ATGGTGACATGGGGGCGCTTGCAACCTGATTCGCAACCGCTTACTCTGACAGGCGCCG 2135
Qy      |||||
21  LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db      |||||
2136  AAGCCTCGACTGTGCAAGAGAAAGCTGCAAGGCGGCGGAGTGTGCTGCGCTGCGCC 2195
Qy      |||||
41  GLYLEUGLNGLYCYALAGLULEUARGLNGLYLEUSERLEUASNPHEHISERLEUCYS 60
Db      |||||
2196  GGGCTGAGGGGCTGGCGGAGCTCCGCAAGAGTGTCCCTGAAGTCTTCCACAGCGCTGT 2255
Qy      |||||
61  GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThr-Phe 80
Db      |||||
2256  GAGCAGAGCGCCATGCTGTGCGCGCTCTTCTCGTGAATCTTCTAGCCACATGCCACGTC 2315
Qy      |||||
81  ARGYSALAAATHRPHLEUGLUASPVAlGlnAsnTPGluLeuAlaGluUuGlyPro 100
Db      |||||
2316  CGCAAGGCGCAACCTTCCTAGAGGAGCGTGAAGACTGGAGTGGCGGAGGAGGCC 2375
Qy      |||||
101  ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db      |||||
2376  ACCAAGACAGCGCGCTGAGGAGGCTGTGCGCACTTGTCGAGTGTGCCCTCCCGGAG 2435
Qy      |||||
121  AAsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrglu 140
Db      |||||
2436  AACCGGCAACCTTCCTGAGCGGAGCGTGTGCGCAACAGTGCAGAGCGACGACCTGAG 2495
Qy      |||||
141  GUUGUARGVALAlaAlaValThrLeuArgValaGluAlaMetAlaPheLeuGlnUu 160
Db      |||||
2496  GAAGAGCGAGTGTGCTGATGACGTGCGCAAGGCTGAGCGCATGCTTCTTGCAAGAG 2555
Qy      |||||
161  GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
Db      |||||
2556  CAGCCTTTAAGATTTCGAGCACAGCGCTTCCTAGACAAATTTCTGCGAGTGAACCTC 2615
Qy      |||||
181  PHEGLUMETGlnProValSerAspLysTrpPheThrGluPheArgValaLeuGlyLysGly 200
Db      |||||
2616  TTGGAGATGCAACAGTGTGACAGAGTACTTCACTGAGTTAGAGTGTGGGAAAGGT 2675
Qy      |||||
201  GLYPHEGLYGLU----- 204
Db      |||||
2676  GGTITTTGGGAGGTAAGTGTCTCCAGTACGAGCTGAGAGGTGAGTAGAGTACAGATGA 2735
Qy      |||||
204  ----- 204
Db      |||||
2736  AAGGGGTAAATGTGCTCTTTTAAATCAAGTTACTTAAGACTAAATTTCAGACAC 2795
Qy      |||||
204  ----- 204

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D 2796 CATATGTGAGGATTTCTAGCCCGTCTCCCAAGCCCTCTTTGTGTGTCAGTG 2855
Q 204 ----- 204
D 2856 TGAATAAACAACAATGCGATGAGAGACAGCAAAATTATCTGGCCAGACTCT 2915
Q 204 ----- 204
D 2916 GTCATGGTCTCCATTAGAAAGTGTGAGATGCTGGACACTTCAGAGATGATGACAA 2975
Q 204 ----- 204
D 2976 TGTGTACAGAGATCTCCGTTTCCCTAAATTGTGATGAGGACTTCAGAAAAA 3035
Q 204 ----- 204
D 3036 TGGATATTTAAGAAAAATCTTAAGCTGGGTGTGTGATGCTGTATCCAGCT 3095
Q 204 ----- 204
D 3096 ACTTGGAGGCTGAAGCAGAGATATCTGAGCTGGAGGTGAGGTTGCACTGAGCC 3155
Q 204 ----- 204
D 3156 AAGATCGTGCACCTGCACTCCAGCTGGGTGACAGACAGACTCAAAAAA 3215
Q 204 ----- 204
D 3216 AAGAAAAAGAAAAAGAAAAACATTATCTGAAGTGAAGTTGAGAACCTGTTTGT 3275
Q 204 ----- 204
D 3276 ACCACTGTTGTGCCAGCTTCTGTTTAAATATAAATAATTTAGGTAAATTTG 3335
Q 204 ----- 204
D 3336 CTGTATATAAATCTAACATTAACTGTTTAAATGTAATGATGATGAGCTTGGACA 3395
Q 204 ----- 204
D 3396 AATGCAATGTGGTGAAGACACTCATCTGATCCAGACACTCTCATGCCCTGT 3455
Q 204 ----- 204
D 3456 GCCCATTAATGTGCTCCCACTCCCTCTCTCTCCAGCCCTGACACCACTAGTCGC 3515
Q 204 ----- 204
D 3516 TTTCTGTCTAGGAAATTGCCATTCGGGTGTTTTCACAAATATGTGACCTTTTGT 3575
Q 204 ----- 204
D 3576 CTGGCTTCTTCACTATTAGAAATGTTTGGGGTTCATTGACAGTGAAGTGTGCA 3635
Q 204 ----- 204
D 3636 TACTCATCTCTTTTATGCGCTGATATAATTCATCGTATGATGATGATGATGATG 3695
Q 204 ----- 204
D 3696 TAGCATTCATCTGTGATGAGACACTGGGCTGTTTTCACCTTTGGCTATGTTGTA 3755
Q 204 ----- 204
D 3756 TGTGTATTTCAGACAGATATTTGTAATCCTGTTTCACTTCTGTGATTTAT 3815
Q 204 ----- 204
D 3816 GCCCAGAGATGATGCTTGAAGCATGTGTATCTATGTTTAACTTTTCAAGAGCA 3875
Q 204 ----- 204

D 3876 CCAAACTTCCACATTTTATTTATCCACAGCAATGCTTAAGTTTCATTTCTCCACA 3935
Q 204 ----- 204
D 3936 TCCCTCCACACTGATATATTTCTGTATTTTATGAGGCTGCTGATGAGTGA 3995
Q 204 ----- 204
D 3996 AAGATATCGACTGATAGTCCCACTTTTCTTGAGAACCTTATTTACAGTACTC 4055
Q 204 ----- 204
D 4056 CTTTCCATAGCTTACATCTTTTCAACCACTCTCTTATCATCTCCACTCTCTG 4115
Q 205 ----- ValCysAla 208
D 4116 CAGTACATCTACTTCTTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4175
Q 208 1GlnValIysAsnThrGlyMetIleAlaCysIleValIleuAspIleValIleu 228
D 4176 CCAAGTAAAAAACAATGAGATGATGCTGTGAGAACTGGACAAAGCGCTGAA 4235
Q 228 sIysIleGlyIleuIleuMetAlaIleuIleuIleuIleuIleuIleuIleuIleu 248
D 4236 GAAGAAAGTGGCAGAGATGCTCTTGAAGAAATCTGAGAAAGTCAAG 4295
Q 248 rProPheIleValSerIleuAlaIleuIleuIleuIleuIleuIleuIleuIleu 268
D 4296 CCGTTATGTTCTCTGCGCTTATGCTTGAAGAACCACTCTGCTGCTGCTGCTGCT 4355
Q 268 tSerIleuMetAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 288
D 4356 GAGCTTATGATGAGGAGACCTCAAGTTCACATTCACAGTGGACCCGTCCT 4415
Q 288 uAspMetSerArgValIlePheIleuIleuIleuIleuIleuIleuIleuIleuIleu 308
D 4416 GAGCATGAGCGGCTGATCTTTTACTGCGCCAGATGAGCTGCGGATCTGACCTCA 4475
Q 308 sGluIleuGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 328
D 4476 TGAACCTGCGATGCTGATGCGGACATGAGGCTGAGATGCTCTGATGATGACCTCG 4535
Q 328 yAsnCysArgIleuSerAspIleuIleuIleuIleuIleuIleuIleuIleuIleu 348
D 4536 CAATGAGGTTATCTGACTGCGGCTGCGGCTGCGGATGAGGATGAGGATGAGGATGAG 4595
Q 348 rGlnArg 350
D 4596 CCAAGG 4602

RESULT 7
US-09-964-469-3
Sequence 3, Application US/09964469
Patent No. 6579709
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000636DIV
CURRENT APPLICATION NUMBER: US/09/964,469
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651
TYPE: DNA
ORGANISM: Human
FEATURE:

NAME/KEY: misc.feature
 LOCATION: (1)...(36651)
 OTHER INFORMATION: n = A,T,C or G
 US-09-964-469-3

Alignment Scores:
 Pred. No.: 1,77e-167 Length: 36651
 Score: 1528.00 Matches: 349
 Percent Similarity: 41.40% Conservativeness: 0
 Best Local Similarity: 41.40% Mismatches: 1
 Query Match: 52.89% Indels: 493
 DB: 4 Gaps: 1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuValAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 2076 ATGTGTGACATGGGGGCTTGGACCACTATGCGCAACACCGCTTACGTGAGGCGG 2135
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 2136 AAGCCCTCGACCTGCGACAGCAAGAGCTGCGAGGCGGCGGCTGAGCTGCGCTGCC 2195
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAspPheHisSerLeuCys 60
 DB 2196 GGGCTGCGAGGCTGCGGAGCTCGCGCAAGAGCTGCTCCCTGAACTTCCACAGCTGTGT 2255
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 DB 2256 GAGCAGACCCCATCGGTGCGGCTGCGCTTCCGTGACTTCCAGCAGTCCACAGTTC 2315
 QY 81 ArgValAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
 DB 2316 CGCAAGCGCGCACTTCTTAGAGGACGTGCAAGAACTGGAGGTGCGCAAGAGGAGCC 2375
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 2376 ACCAAGACAGCGCGCTGCGAGGCTGTGGCGCACTTGTCCAGTCCCTGCGCGGCGG 2435
 QY 121 AspProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 2436 AACCCGCACTTCTTCTAGCGCGCGCTGCGCAAGAGTCCAGCGCGCCACACCTGAG 2495
 QY 141 GluLysArgValAlaAlaValAlaThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 2496 GAAGAGCGAGTGGCTGCGAGTGAACCTGCGCAAGGCTGAGGCTGCTTCTGCAAGAG 2555
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 DB 2556 CAGCCCTTTAAGGATTTGCGACAGCGCTTCTACAGCAAGTTCTGCAAGTGAACCTC 2615
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 DB 2616 TTCAAGATGGAACAGAGTGTGACACAGTACTTCACTGAGTTCAGAGTGTGCGGAAAGGT 2675
 QY 201 GlyPheGlyGlu----- 204
 DB 2676 GGTTTGGGAGGTAAAGTGTCTCCAGTAGCCAGGCTAGAAAGTGAAGCATAGACATGA 2735
 QY 204 ----- 204
 DB 2736 AAGGGGGTAATGTGCTTCTTTTAAATCTCAATTACTTAGAACTAATTTAGACAC 2795
 QY 204 ----- 204
 DB 2796 CATATGTGAGGATTTCTAGCCCGTCTCCAGCCCTTCTTTGTGTGTCATGTGTG 2855
 QY 204 ----- 204
 DB 2856 TGAATATAAACAAATGCGATGAGAGAGCAAGCAAAATTATTACTTGCCCAAGACTCT 2915
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DB 2916 GTCATGGCTTCCATTAGAGAGCTGCAAGTGCCTGACACTTCAAGAAATGATGCAA 2975
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 DB 2976 TGTGTACAGAAAGATCTCGGTTCCCTTAATGTGTATATGAAAGCACTTCAAGAAAA 3035
 QY 204 ----- 204
 DB 3036 TGGATATTTAAGAAAAATTAATCTTAAGTACGTGGGTGTGATGATGCTGTATCCAGCT 3095
 QY 204 ----- 204
 DB 3096 ACTTGGAGGCTGAAGCAAGAGAAATCACTTGAAGCTGGAGGTGGAGGTTCAGATGACC 3155
 QY 204 ----- 204
 DB 3156 AAGATGTGTGCACTGCACTCCAGCTGGGTGACAGACAGACTCAAAAAAAAAAAAAA 3215
 QY 204 ----- 204
 DB 3216 AAGAAAGAAAAAGAAAAAGAAAAACCTTAATCTGAAGTAAGGTGAGAACTGTGTTGT 3275
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 DB 3276 ACCAGTGTGTGCCAGCTTCTGTGTTTAAGTAATAAAAAATTTAGGTAAATTTG 3335
 QY 204 ----- 204
 DB 3336 CTGTATATAAACTAACCATTAATCTGTTTAAATATGATGACATGAGTGGCACTTGGACA 3395
 QY 204 ----- 204
 DB 3396 AATGCAATGTGGGTAAAGCAACCTCAATCTGATTCAGACACTCTATACCCCTGT 3455
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 DB 3456 GCCATTAAATAGTCTCCCTCCATCCCTCTCTCCAGCCCTGACAACTAGTCCGC 3515
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 DB 3516 TTCTGTCTAGGATTTGCTATCTGGGTGTTTCACAGATATGTGACCTTTGTGT 3575
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 DB 3576 CTGGCTCTTTCACCTAATGAATGTTTTGGGCTTCACTACACTGATGATGTGCA 3635
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 DB 3636 TACTCAATCTTTTATGTGCTGTATTAATTTCCATGATGATGATGATGATGATGATG 3695
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 DB 3696 TAGCATTCATCTGTGATGATGACTGAGCTGTTCACCTTTGGCTATGTGTATG 3755
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 DB 3756 TGTGTATTCATGACCAAGTATTTGTTGAATCTTGTTCATTTCTGTGATTTAT 3815
 QY 204 ----- 204
 DB 3816 GCCAGAGTGAATTGCTAGGCAATGATGATGATGATGATGATGATGATGATGATGATG 3875
 QY 204 ----- 204
 DB 3876 CCAACTTTCCACATTTTATTTCCACACAGCAATGCTTAAAGTTTGATTTCTCACA 3935
 QY 204 ----- 204
 DB 3936 TCCCTGCAACCTGATATTTTCTGTATTTTATTAAGGCTGCTAGTGAAGTGA 3995
 QY 204 ----- 204
 DB 3996 AGAGATGCGACGTGTATGCCACTTTTCTGTAGAACTTTATTTAATTAACGCTACTC 4055

QY 204 ----- 204
 Db 4056 CTTTCAGATGCTAATCTTTCCACCACTCTCTTATCATCTCAACCTCTCTG 4115
 QY 205 -----ValCySAIaVa 208
 Db 4116 CAGTACCATCTACTTCTACCTCTTCTCTTTCTTTCTCTTTAAAGTATGCGCT 4175
 QY 208 1GlnValIysAsnThrGlyIysMetIYrAlaCysIysIysLeuAspIysIYrAsnLeuIY 228
 Db 4176 CCGGTGAAAAACACTGGGAGATGATGCTCTGAGAAACTGCAAGAAAGCGGCTGAA 4235
 QY 228 sIYsIYsGlyIYsIYsMetAlaIleuIYsGlnIleuIYsIYsValSerSe 248
 Db 4236 GAAAGAAAGTGGCGGAGAAAGTGGCTCTCTGAGAAAGAAATCTTGAGAAAGCTGACAG 4295
 QY 248 rProPheIleValSerIleuAlaIYrAlaPheGlySerIYsThrHisIleuIYsIleuIYs 268
 Db 4296 CCTTCATGTCCTCTCTGGGCTATGCTCTTGAAGCAAGAACCAATCTCTGCTGTCTCAT 4355
 QY 268 tSerIleuMetAsnGlyIYsIYsPheHisIleYrAsnValGlyThrArgIYsIYs 288
 Db 4356 GAGCTCGATGATGGGGAGACCTCAAGTTCACATCTCAACGTCGGCAAGGTGGCT 4415
 QY 288 uAspMetSerArgValIlePheIYrSerAlaGlnIleAlaCysGlyMetIleuHisIleuH 308
 Db 4416 GGAATGAGCCGGGTGATCTTTACTCGGCGCAAGATGCGCTGTGGGATCTGCACTTCCA 4475
 QY 308 sGlnIleuGlyIleValIYrAsnPheIYsProGlnuAsnValIleuIYsAspIleuI 328
 Db 4476 TGAATCGGCATCGCTATGCGGACATGAAACCTGGAATGTGCTTCTGATGACCTTGG 4535
 QY 328 YAsnCysArgIleuSerAspIleuIYsAlaIYsIleuIYsGlyIYsProIleuH 348
 Db 4536 CAACGTGCAAGTTATCTGACCTGGGGCTGGCGTGAAGTGAAGGGTGGCAAGCCCATGAC 4595
 QY 348 rGlnArg 350
 Db 4596 CCGAGAG 4602
 RESULT 8
 US-09-614-748A-7
 ; Sequence 7, Application US/09614748A
 ; Patent No. 6660474
 ; GENERAL INFORMATION:
 ; APPLICANT: FELDER, ROBIN A.
 ; TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
 ; FILE REFERENCE: FELDER 3-9-001 CONT
 ; CURRENT APPLICATION NUMBER: US/09/614,748A
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: PCT/US99/00663
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/071,199
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/098,279
 ; PRIOR FILING DATE: 1998-08-28
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 2113
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-614-748A-7
 Alignment Scores:
 Pred. No.: 2,28e-140
 Score: 1280.50
 Percent Similarity: 65.49%
 Best Local Similarity: 47.39%
 Query Match: 44.32%
 Length: 2113
 Matches: 254
 Conservative: 97
 Mismatches: 162
 Indels: 23

DB: 4 Gaps: 8
 US-10-044-205a-2 (1-553) x US-09-614-748A-7 (1-2113)
 QY 7 LeuAspAsnIleuIleAlaAsnThrAlaTYrLeuGlnAlaArgIYsProSer----AspCys 25
 Db 261 CTGAGAAACATCGGTGCGCAACTCGCTGCTGTAAGAGCGGTCAAGAGAGATGTGGCAAA 320
 QY 26 AspSerIYsGlnIleuIYsIYsArgIYsSerIleuAlaIleuProGlyIleuGlnIYs 45
 Db 321 AAAAGTGTGTGTAATAAAATGAAAGAGATCTGACACTGCTCTGCTGACCGCAGTGC 380
 QY 46 AlaGlnIleuArgIYsIleuSerIleuAsnPheHisSerIleuIYsGlnIYsIleuIYs 65
 Db 381 AGTGAAGCTTGACATTCATTCATGAAAGATTTAGACGCTTTGTGACAGAACCGATA 440
 QY 66 GlnArgArgIleuPheArgAspPheIleuAlaThrValProThrPheArgIYsAlaThr 85
 Db 441 GGAAGAGCTCTCTTCAGGACGCTGATGATGACCAACCACTCAAGAGGCACTTGA 500
 QY 86 PheIleuIYsIYsAlaGlnAsnIYrGlnIleuAlaGlnIYsIYsProThrIYsAsp----- 103
 Db 501 TTTTGATGCACTGCGCAGAAATGAAAGTGGCGATGATGAGACGCAAGTATGTGGA 560
 QY 104 ---SerAlaIleuGlnIYsIleuValAlaThrCysAlaSerAlaProIYsAsnPro 122
 Db 561 CTGTCAATCTTGATGATGATTTCTCATGATGATGATGATGATGATGATGATGATGAT 620
 QY 123 GlnProPheIleuSerGlnAlaIleuIYsCysGlnAlaIleuIYsIleuIYsIleuIYs 142
 Db 621 CCAAGT-----GTTGTCAGAGAAATGAAATGTTGGGACTGAGAGAGAGAAAC 665
 QY 143 ArgValAlaIleuValThrIleuArgIYsAla-----GlnAlaMetAla 156
 Db 666 -----CCTTCGAAAAAGCCTTGGAGATGTACTGAGATGTCGCAATGTCCTCATAC 710
 QY 157 PheIleuGlnIYsIleuProPheIYsAspPheValThrSerAlaPheIYsIleuIYs 176
 Db 711 TACCTAAGAGGGAACCTTTGAAGATGACCAAGAAAGCTCATATTTTCTCAAGTTTGA 770
 QY 177 GlnIYrIYsIleuPheGlnIleuIYsIleuIYsIleuIYsIleuIYsIleuIYsIleuIYs 196
 Db 771 CAATGAAATGCTGGAAGAGCAACCCGTTACCAAGAAACATTTAGCATTAAGAGTT 830
 QY 197 LeuIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYs 216
 Db 831 CTAGAAAAAGGCGATTTGAGAGGTTGCGCTGTCAGATGCGCAGCAAGAAAAAG 890
 QY 217 TYrAlaCysIYsIYsIleuAspIYsIYsArgIleuIYsIYsIYsIYsIYsIYsIYsIYs 236
 Db 891 TATGCTGCAAAAAGCTTCAAAAAGATTTAGAAAGAGAAAGAGGAGGCTTATGCT 950
 QY 237 LeuIleuGlnIYsGlnIleuIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYs 256
 Db 951 CTAAATGAGAAAAAATTTGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1010
 QY 257 AlaPheGlnIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYs 276
 Db 1011 GCTTATGAAACCAAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
 QY 277 IYsPheHisIleYrAsnValGlyThrArgIYsIleuAspMetSerArgValIlePheIYr 296
 Db 1071 AAGTTCACTTCAACCTGCGCAATCCGAGCTTTGATGACAGAGACCGCTTTCTAT 1130
 QY 297 SerAlaGlnIleAlaCysGlyMetIleuHisIleuIYsGlnIleuGlyIleValIYrAsp 316
 Db 1131 GCTGCAAGAGCTGTGCTGCGCTTGAAGATTTACAGAGGAAAGATTTGATACAGAGAC 1190
 QY 317 MetIYsProGlnuAsnValIleuIYsAspIleuIYsIYsIYsIYsIYsIYsIYsIYsIYs 336
 Db 1191 TTGAAGCTGAGAAATTTCTCTTGAAGTGTGAGCAATCCGAAATTTGACCTCGCT 1250
 QY 337 LeuAlaValIleuIYsGlyIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYsIYs 356

[illegible]


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Db      1738  TCAAGCTGGCTTGGCTGTGAAGATCCCGAGGAGACCTGATCCGGCGCGGTGGCC 1797
Qy      353  ThransglyTyrMetAlaProGluIleLeuMetGluValSerTyrSerTyrProVal 372
Db      1798  ACTGTGGCTTACATGCCCCCGAAGCTCTGAACACGCG---AGGTACGGCTGAGCCCC 1854
Qy      373  AspTyrPheAlaMetGlyCysSerTyrGluMetValAlaGlyThrProPheLys 392
Db      1855  GACTACTGGGCTTGGCTGGCTCATCTATGATGATGAGGCGGCGGCTGGCTGGC 1914
Qy      393  AspTyrLysGluLysValSerTyrGluAspLeuLysGluArgThrLeuGluAspGlu 412
Db      1915  GGCCCTAGAGAGAGGTGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1974
Qy      413  LysPheGlnHisAspAsnThrGluGluAlaLysAspIleCysArgLeuPheLeuAla 432
Db      1975  GTGTACTCCAC---AAGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2031
Qy      433  LysLysProGluGlnArgLeuLysSerTyrGluLys---SerAspAspProArgLysHis 451
Db      2032  AAGATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2091
Qy      452  HisPhePheLysThrIleAsnThrProArgLeuGluAlaGlyLeuIleGluProPhe 471
Db      2092  CCTCTCTTCAGAGAACATGAATTCAGAGGCTTGAAGCGGAGATGTTGACCTCCCTC 2151
Qy      472  ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
Db      2152  GTTCCAGACCCCGCGCTGTGTACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2211
Qy      492  ValArgIleValGluPheAspAspLysAspLysGluPheLysAsnPheAlaThrGly 511
Db      2212  GTGAGAGGGGTGCATCTGCAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2271
Qy      512  AlaValProIleAlaThrGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
Db      2272  TCTGTCTCATCTCCATGCAAAACAGATGATGAAGAGAGAGAGAGAGAGAGAGAG 2331
Qy      532  -----AspPro-AsnArg 535
Db      2332  GTGTTTGACCTAATGTAACCTCCCGCAATCTGAACAGAAACCACTCCGGAACCG 2391
Qy      535  gPro--ThrglyCysGluGluLysAsnSerLysSer 547
Db      2392  CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCGAGC 2431

RESULT 11
US-09-016-434-1298
; Sequence 1298, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1298:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g306804
; US-09-016-434-1298

Alignment Scores:
Pred. No.: 6,19e-137 Length: 2557
Score: 1252.50 Matches: 259
Percent Similarity: 63.07% Conservative: 103
Best Local Similarity: 45.12% Mismatches: 162
Query Match: 43.35% Indels: 50
DB: 4 Gaps: 11

US-10-044-205A-2 (1-553) x US-09-016-434-1298 (1-2557)

Qy      7  LeuAspAsnLeuIleAlaSerThrAlaTyrLeuGluAlaArgLysProSerAspCysAsp 26
Db      227  CTGGAATAAATCTGTGGCCACACGCGTCTGCGAAGCGAAGAGAGAGAGAGAGAGAG 286
Qy      27  SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
Db      287  CGCAAGAGGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 346
Qy      46  AlaGluLeuArgGlnLysLeuSerLeuAsnThrHisSerLeuCysGluGlnProIle 65
Db      347  GAAAGACCTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 406
Qy      66  GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
Db      407  GGGAGGCTGCTTTTCCGGCAGTTTGTGAACACAGGCGCTGGAGGTGAATTCAG 466
Qy      86  PheLeuGluAspValGlnAsnTyrGlu-----LeuAlaGluGluGly 99
Db      467  TTCCTGAGACTCCGTGGCAGAAATATGAGTTACTCCAGATGAAACCTGGAGAGAGAG 526
Qy      100  ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
Db      527  -----AAGGAATTTATGACCAAGTACTC-----ACCCA 556
Qy      120  GlyAsnPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
Db      557  AAGTCCCTGTTTTCATACCCAGAGTTGGCAGAGACTGGCTCCACAGAGAGAGAGAG 616
Qy      133  LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
Db      617  CTCCTACAGAAAGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 673
Qy      153  GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
Db      674  -----TACCTGAGGGGAGAGACATTCACAGATATCTGAGCAGAGATTTT 721
Qy      173  AspLysPheLeuGlnTyrLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
Db      722  GACCGCTTCTCCAGGTGAGAGAGGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
Qy      193  GluPheArgValLeuGlyLysGlyLysPheGlyValCysAlaValGlnValLysAsn 212

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Db      782  CAGATGAGTCTCTAGAGAGAGGAGGCTTCGGGAGGCTGTGCTCCAGGCTTCGGGCGC 841
QY      213  ThGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyGly 232
Db      842  ACGGGTAATATGATGCTCGCAAGCCCTGGAGAGAGAGAGATCAAAAAGAGAGAGG 901
QY      233  GlnLysMetAlaLeuLeuGlnLysGlnLysLysLysValSerSerProPheIleVal 252
Db      902  GAGTCATGCGCTTCATGAGAGAGAGATCTCCAGAGAGGCTCAACAGTCAGTTTGTC 961
QY      253  SerLeuAlaTyrAlaPheGlnSerLysThrHisLeuCysLeuValMetSerLeuMetAn 272
Db      962  AACCTGCTATGCTCTGAGAGACCAAGATCCATGCTGCTGCTGCTCAACATCAAT 1021
QY      273  GlyLysAspLeuLysPheHisIleTyrAsnValGlyThrArgLysLeuMetSerArg 292
Db      1022  GGGGTCGACCTGAGAGTTCACATCTCAACATGAGGACCCGCTTCAGAGAGAGCGG 1081
QY      293  ValLysPheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlnLeuGly 312
Db      1082  GCGCTGTTTATGCGGAGAGATCTCTGCGGCTTGAAGACCTCAACCGTGAAGAAC 1141
QY      313  ValTyrArgAspMetLysProGlnAsnValLeuLeuAspLeuGlnLysCysArgLeu 332
Db      1142  GTCTACCAAGATCTGAAGACCTGAAGACCTCTGTGATGATTTGCGCCATTAGGATC 1201
QY      333  SerAspLeuGlnLysLeuAlaValGlnMetLysGlyLysProLysThrGlnAlaGly 352
Db      1202  TCAGACTGGGCTGTGCTGTAAGATCCCGAGAGGAGACCTGATCCGCGCGGAGGCG 1261
QY      353  ThrAsnGlyTyrMetAlaProGlnIleLeuMetGlnLysValSerTyrSerTyrPro 372
Db      1262  ACTGTTGCTATGAGCGCCCGAGATCTCTCAACACAG---AGGTAGCGCTGAGCC 1318
QY      373  AspTyrPheAlaMetGlyCysSerLysLeuGlnMetValAlaGlyArgThrProPhe 392
Db      1319  GACTACGTGGGCTTGGCTGCTCTCATCTATGATATGATGAGGCGAGTGGCGCTCC 1378
QY      393  AspTyrLysGlnLysValSerLysGlnAspLeuLysGlnArgThrLeuGlnAspVal 412
Db      1379  GCGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
QY      413  LysPheGlnHisAspAsnPheThrGlnGlnAlaLysAspIleCysArgLeuPheLeu 432
Db      1439  GTGTATCTCCAC---AAGTTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1495
QY      433  LysLysProGlnGlnArgLeuGlnSerArgLysLys---SerAspAspProArgLys 451
Db      1496  AAGATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1555
QY      453  HisPhePheLysThrIleAsnPheProArgLeuGlnAlaGlnLeuIleGlnProPhe 471
Db      1556  CCTCTTTCAGAGAACTGAATCAACGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 1615
QY      472  ValProAspProSerValValTyrAlaLysAspIleAlaGlnIleAspAspSerGln 491
Db      1616  GTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675
QY      492  ValArgGlyValGlnPheAspAspLysAspLysGlnPhePheLysAsnMetAlaThr 511
Db      1676  GTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1735
QY      512  AlaValProIleAlaTyrGlnGlnGlnIleIleGlnThrGlnLeuPheGlnGln 531
Db      1736  TCTGTGTCATCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1795
QY      532  -----AspPro-AsnAr 535
Db      1796  GTGTTTGACCTTAAGGTACCTCCGCGAGATCTGAACAGAGAGAGAGAGAGAGAG 1855
QY      535  gPro---ThrGlyCysGlnGlnGlnLysSerSerLysSer 547

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Db      1856  CCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1895
RESULT 12
US-09-614-748A-9
Sequence 9, Application US/09614748A
Patent No. 6660474
GENERAL INFORMATION:
APPLICANT: FELDER, ROBIN A.
APPLICANT: JOSE, PEDRO
TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
FILE REFERENCE: FELDER 3.9-001 CONT
CURRENT APPLICATION NUMBER: US/09/614,748A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: PCT/US99/00663
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/071,199
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/098,279
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 1975
TYPE: DNA
ORGANISM: Homo sapiens
US-09-614-748A-9
Alignment Scores:
Pred. No.: 6,96e-137 Length: 1975
Score: 1250.50 Matches: 250
Percent Similarity: 64.95% Conservative: 91
Best Local Similarity: 47.62% Mismatches: 161
Query Match: 43.28% Indels: 23
Gaps: 8
US-10-044-205A-2 (1-553) x US-09-614-748A-9 (1-1975)
QY      7  LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer--AspCys 25
Db      261  CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 320
QY      26  AspSerLysGlnLeuGlnArgArgSerLeuAlaLeuProGlnLysGlnGlnGlyCys 45
Db      321  AAAAGGCTGCTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY      46  AlGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGlnGlnGlnProIle 65
Db      381  AGTAGAGCTTAACTTCATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
QY      66  GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
Db      441  GGAAGAGCTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
QY      86  PheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyProThrLysAsp----- 103
Db      501  TTCTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
QY      104  ---SerAlaLeuGlnGlnLysValAlaThrCysAlaSerAlaProAlaProGlnAsnPro 122
Db      561  CTGTCAATCTTATGATGATTTCTTCAATGATTAAGTTAGAGAGAGAGAGAGAGAGAG 620
QY      123  GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaAlaThrThrGlnGln 142
Db      621  CCAAGT-----GTTGTGACAGAAATGATTTGGAGCTGAAGAGAGAGAGAGAGAG 665
QY      143  ArgValAlaAlaValThrLeuArgLysAla-----GlnAlaMetAla 156
Db      666  -----CCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
QY      157  PheLeuGlnGlnGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
Db      711  TACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 770

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QY 177 GlnTrpLysLeuPheGlnMetGlnProValSerAspLysTrpPheThrGlnPheArgVal 196
Db 771 CAATGGAAATGGCTGGAAAGCAACCGTGAACAAAGAAACACATTAGACATTAAGAGATT 830
QY 197 LeuGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 216
Db 831 CTAGGAAAGCGGATTTGGAGAGGTTGGCTGTCATAGCCAGCCACGAGGAAAGATG 890
QY 217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyGlyGlyGlyGlyGlyGly 236
Db 891 TATGCTCTGCAAAAAGCTCAAAAAGAAATAGAGAGAGAAAGGATGAGCTATGCT 950
QY 237 LeuLeuGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 256
Db 951 CTAATAGAGAAAGAAATCTGAGAGAAAGTCAAGAGTAATTCGATGATGATGATGATGAT 1010
QY 257 AlaPheGlySerLysThrHisLeuGlyLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
Db 1011 GCTTATGAAACCAAAAGATGCTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
QY 277 LysPheHisLysLysValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 296
Db 1071 AAGTTTCAATTAACAAACCTGGGCAATCCGGCTTGTGATGAGCAGAGAGCGCTTTCTAT 1130
QY 297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlyGlyGlyGlyGlyGlyGlyGly 316
Db 1131 GCTGAGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
QY 317 MetLysProGlyLysValLeuLeuAspLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 336
Db 1191 TTGAAGCTGAGATATCTCTCTTATATGTCGACACATCCGATTTGAGCCCTCGCT 1250
QY 337 LeuAlaValGlyMetLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 356
Db 1251 TTGGGCAAGAGATCCAGAGAGACAGAGGCTTGCAGAGAGAGCTTGCAGAGAGCTTGC 1310
QY 357 MetAlaProGlyLysLeuMetGlyLysValSerLysTrpProValAspTrpPheAla 376
Db 1311 ATGGACCTGAGAGTTCATATATGAA--AAGTATACGTTTATGCTCCGATGATGAGGGA 1367
QY 377 MetGlyCysSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 396
Db 1368 CTGGCTGCTGATCTTGAATGATTCAGGAGATTTCTCCATTCAGAAATTCAGAAAG 1427
QY 397 LysValSerLysGlyAspLeuLysGlnArgThrLeuGlnAspGlyValLysPheGlnHis 416
Db 1428 AAGTCAATGGAGAGAGGTCATCAAGAAATCAAGATGATGATGATGATGATGATGATGAT 1484
QY 417 AspAsnPheThrGlnGlyLysAlaValAspLysLeuGlyLeuPheLeuAlaLysLysProGly 436
Db 1485 GAGAGATTTTCAGAGAGATGCAATCTGTCAGGATGTCATGATGATGATGATGATGATGAT 1544
QY 437 GlnArgLeuGlySerArg--GlyLysSerAspAspProArgLysHisHisPhePheLys 455
Db 1545 AAGCGCTGAGCTGAGAGGCGAGGAGGAGGCTGGGCTGAAGAGACCCGCTGTTCAAG 1604
QY 456 ThrIleAsnPheProArgLeuGlnAlaGlyLysLeuGlyProPheValProAspPro 475
Db 1605 GACATCACTTCAGAGAGCTGAGAGCAACATGCTGAGAGCCCTTTCTGCTGATGCT 1664
QY 476 SerValValTyrAlaLysAspIleAlaGlnLeuAspPheSerGlyValArgGlyVal 495
Db 1665 CATGCCGTTTACTGTAAAGAGCTGCTGATTCAGAGATTCCTGCGCGCTAAAGGAGATC 1724
QY 496 GlnPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
Db 1725 TACCTGAGACCGCAGATGAAGACTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1784
QY 516 AlaTrpGlnGlnGln 520
Db 1785 CCTGGCAGATGAG 1799

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RESULT 13
US-09-614-748A-8
; Sequence 8, Application US/09614748A
; Patent No. 6660474
; GENERAL INFORMATION:
; APPLICANT: FELDER, ROBIN A.
; APPLICANT: JOSE, PEDRO
; TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: FELDER 3.9-001 CONT
; CURRENT APPLICATION NUMBER: US/09/614,748A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: PCT/US99/00663
; PRIOR FILING DATE: 1999-01-12
; PRIOR FILING DATE: 60/071,199
; PRIOR APPLICATION NUMBER: 60/098,279
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2017
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-748A-8

Alignment Scores:
Pred. No.: 4,81e-136 Length: 2017
Score: 1243.50 Matches: 248
Percent Similarity: 62.99% Conservative: 89
Best Local Similarity: 46.36% Mismatches: 145
Query Match: 43.04% Indels: 53
DB: Gaps: 8

US-10-044-205A-2 (1-553) x US-09-614-748A-8 (1-2017)
QY 7 LeuAspAsnLeuIleAlaSerThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
Db 261 CTCGAGAACTGCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
QY 27 SerLysGlnLeuGlnArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCysAla 46
Db 314 ----- 314
QY 47 GlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuGlyGlnGlnProIleGly 66
Db 315 -----TATACAGCTTTTGTGCAAGCAACGATGAGA 347
QY 67 ArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThrPhe 86
Db 348 AGAGCTCTTTCAGCAGAGTCTGATGATCCAAACCACTCTTAAAGAGGACATGGAATTC 407
QY 87 LeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyProThrLysAsp----- 103
Db 408 TTGATGCACTGAGCAATATGAAATGTTGCGGATGATGAGAGCCAGATGTTGAGACTG 467
QY 104 SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnProGln 123
Db 468 TCAATCTTAATGATGATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527
QY 124 ProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlnGlnGlnArg 143
Db 528 GAT-----GTTGTGACAGAAATGTAATGAGGAGCTGAAAGAGAGAGAAC--- 569
QY 144 ValAlaAlaValThrLeuArgLysAla-----GlnAlaMetAlaPhe 157
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; Sequence 2, Application US/08464954A
; Patent No. 6255069
; GENERAL INFORMATION:
; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
; APPLICANT: PRITA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076,084
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0118
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2848
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-464-954A-2
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 14:01:20 ; Search time 692.966 Seconds
(without alignments)

15563.146 Million cell updates/sec

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Perfect score: 2198

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapept 1.0

Searched: 3225727 seqs, 245303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	1658.4	75.5	1662	15 US-10-217-745-1
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16	401.6	18.3	2817	15 US-10-388-934-621	Sequence 621, App
17	379.4	17.3	2467	15 US-10-084-817-110	Sequence 110, App
18	377.8	17.2	2519	14 US-10-071-766-13	Sequence 13, Appl
19	374.6	17.0	2519	10 US-09-971-392-72	Sequence 72, Appl
20	373	17.0	2511	15 US-10-072-036-60	Sequence 60, Appl
21	373	17.0	2529	15 US-10-072-036-42	Sequence 42, Appl
22	373	17.0	2557	9 US-09-972-694-1	Sequence 7, Appli
23	373	17.0	2557	12 US-10-380-235-7	Sequence 1, Appli
24	373	17.0	2557	16 US-10-305-720-1298	Sequence 1298, Ap
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28	158.4	7.2	493	10 US-09-818-995-37835	Sequence 37835, A
29	153.4	7.0	3154	10 US-09-955-999-45	Sequence 25, Appl
30	151	6.9	1679	9 US-09-771-161A-25	Sequence 25, Appl
31	151	6.9	2037	13 US-10-087-684-23	Sequence 23, Appl
32	151	6.9	2037	13 US-10-218-779-23	Sequence 47, Appl
33	151	6.9	2070	15 US-10-038-010-47	Sequence 11, Appl
34	151	6.9	3073	13 US-10-029-020-11	Sequence 3, Appli
35	151	6.9	3268	15 US-10-247-671-3	Sequence 482, App
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44	127.6	5.8	2362	16 US-10-117-722-273	Sequence 273, App
45	112.4	5.1	1661	13 US-10-087-192-989	Sequence 989, App

ALIGNMENTS

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Sequence 1, Application US/10044205A
Publication No. US20020123464A1
GENERAL INFORMATION:
APPLICANT: KAPLELLER, LIBERMAN, Rosana
APPLICANT: BANDARU, Rajasekhar
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044,205A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/241,884
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,877
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2198
TYPE: DNA
ORGANISM: Homo sapiens
US-10-044-205a-1

Query Match 100.0%; Score 2198; DB 14; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1141	GCACGCTGACCTGACATGAGCCGGATCTTTTACTGGCCAGATACCTGTGGGA	1200
DB	1141	GCACGCTGACCTGACATGAGCCGGATCTTTTACTGGCCAGATACCTGTGGGA	1200

QY	1201	TGTCGACCTCCATGAACTCGGCACTCGCTATCGGGACATGAAGCTCGAAGTGTCTTC	1260
Db	1201	TGTCGACCTCCATGAACTCGGCACTCGCTATCGGGACATGAAGCTCGAAGTGTCTTC	1260
QY	1261	TGATGAACTCGGGCACTGCAAGGTTATCTGACTCTGAGCGCTGCGTGGAGATGAAGGCTG	1320
Db	1261	TGATGAACTCGGGCACTGCAAGGTTATCTGACTCTGAGCGCTGCGTGGAGATGAAGGCTG	1320
QY	1321	GCAAGCCATCAACCCAGAGGGCTGGAACCAATGGTTCAATGGCTCGTGAATCTTAATGG	1380
Db	1321	GCAAGCCATCAACCCAGAGGGCTGGAACCAATGGTTCAATGGCTCGTGAATCTTAATGG	1380
QY	1381	AAAAGGTAAGTATTCCTAATCTGTGAACTGGATTGCAATGGGATGCAATTTATGAA	1440
Db	1381	AAAAGGTAAGTATTCCTAATCTGTGAACTGGATTGCAATGGGATGCAATTTATGAA	1440
QY	1441	TGGTGTCTGAGAAACACCAATTCMAAGATTACAGAAAAGTCTGCTAAAGAGATCTGA	1500
Db	1441	TGGTGTCTGAGAAACACCAATTCMAAGATTACAGAAAAGTCTGCTAAAGAGATCTGA	1500
QY	1501	AGCAAGATCTTCGCAACAGAGTGAATTCAGACATGATTACTTCACAGAGAGCA	1560
Db	1501	AGCAAGATCTTCGCAACAGAGTGAATTCAGACATGATTACTTCACAGAGAGCA	1560
QY	1561	AAAGATTTTCAGAGCTCTTCTTGCTTAAGAAACAGCAAGCTTAAAGAACAGAGAA	1620
Db	1561	AAAGATTTTCAGAGCTCTTCTTGCTTAAGAAACAGCAAGCTTAAAGAACAGAGAA	1620
QY	1621	AGTCTGATATCCAGAGAAACATATTTCTTTAAAGATCACTTCCTCGCTGGAG	1680
Db	1621	AGTCTGATATCCAGAGAAACATATTTCTTTAAAGATCACTTCCTCGCTGGAG	1680
QY	1681	CTGGCTTAATGAAACCCCATTTGTGCGAGACCTTCAGTGGTTATGCGAAGACATG	1740
Db	1681	CTGGCTTAATGAAACCCCATTTGTGCGAGACCTTCAGTGGTTATGCGAAGACATG	1740
QY	1741	CTGAATATGATATTTCTCTAGAGTTGCGGGGGTGGAAATTGATGACAAAGATGAAGAGT	1800
Db	1741	CTGAATATGATATTTCTCTAGAGTTGCGGGGGTGGAAATTGATGACAAAGATGAAGAGT	1800
QY	1801	TCTTCAAAAACTTTTGGCAAGGTGTGTCTTAAGCATGCGACAGAAAGAAATTTATGAA	1860
Db	1801	TCTTCAAAAACTTTTGGCAAGGTGTGTCTTAAGCATGCGACAGAAAGAAATTTATGAA	1860
QY	1861	CGGGACTGTTGAGAGAACTGAATGACCCCAACAGACTACGAGTTGTAGAGGGTATT	1920
Db	1861	CGGGACTGTTGAGAGAACTGAATGACCCCAACAGACTACGAGTTGTAGAGGGTATT	1920
QY	1921	CATCAAGTCTGCGGTGTGTTTATTGTAAATTCCTCTTACACAGAGGACAG	1980
Db	1921	CATCAAGTCTGCGGTGTGTTTATTGTAAATTCCTCTTACACAGAGGACAG	1980
QY	1981	GAGTCTCGGCTGACATAATCTCGAATTTTCAACAGTGGAAATCTGTGAATGAGGCT	2040
Db	1981	GAGTCTCGGCTGACATAATCTCGAATTTTCAACAGTGGAAATCTGTGAATGAGGCT	2040
QY	2041	AATCAGTTAGAGGAGACATCAACACCAAAACAAATTCAAAAGACAGCAAGCTCAAC	2100
Db	2041	AATCAGTTAGAGGAGACATCAACACCAAAACAAATTCAAAAGACAGCAAGCTCAAC	2100
QY	2101	TAGAACATTTAATTTCTTTCTTTCTCATAAAGATGAATGAAGTCAAGTTTCA	2160
Db	2101	TAGAACATTTAATTTCTTTCTTTCTCATAAAGATGAATGAAGTCAAGTTTCA	2160
QY	2161	CTGAGGCGAGGAAAGAAACACTCAGGTTTATTTTGA	2198
Db	2161	CTGAGGCGAGGAAAGAAACACTCAGGTTTATTTTGA	2198

Qy	711	GAAGACGAGTGCCTGCAGTGAACGCTGGCGAAAGGCTGAGCCATGAGCTTCTCTGCAAGG	770
Db	421	GAAGACGAGTGCCTGCAGTGAACGCTGGCGAAAGGCTGAGCCATGAGCTTCTCTGCAAGG	480
Qy	771	CAGCCCTTTAAGATTTTCGTGACCAAGCCCTTCTACGACAAAGTTTCTGAGTGAATCTC	830
Db	481	CAGCCCTTTAAGATTTTCGTGACCAAGCCCTTCTACGACAAAGTTTCTGAGTGAATCTC	540
Qy	831	TTGAGATGCACACAGTGTGCACAAAGTACTTCACTGATTCAGAGTGCCTGGGAAAAGGT	890
Db	541	TTGAGATGCACACAGTGTGCACAAAGTACTTCACTGATTCAGAGTGCCTGGGAAAAGGT	600
Qy	891	GCTTTTGGGAGATATGTGCGCTGCACAGTGAAGAAAACACTGGGAAATGTATGCTCTAAG	950
Db	601	GCTTTTGGGAGATATGTGCGCTGCACAGTGAAGAAAACACTGGGAAATGTATGCTCTAAG	660
Qy	951	AAACTGGACAAAGACGGCTGGAAGAAAGGTGGCGAGAAAGTGGCTCTCTTGGAAAG	1010
Db	661	AAACTGGACAAAGACGGCTGGAAGAAAGGTGGCGAGAAAGTGGCTCTCTTGGAAAG	720
Qy	1011	GAATCTTGGAGAAGGTGACGAGCCCTTCAATTGTCTCTCTGACCTATGCTTTGAGAG	1070
Db	721	GAATCTTGGAGAAGGTGACGAGCCCTTCAATTGTCTCTCTGACCTATGCTTTGAGAG	780
Qy	1071	AAGACCATCTGCGCTGTGTACAGACCTGATGAATGGGGGAGACCTCAAGTTCCATC	1130
Db	781	AAGACCATCTGCGCTGTGTACAGACCTGATGAATGGGGGAGACCTCAAGTTCCATC	840
Qy	1131	TTCAACGAGGACACGGTGGCTGACATGACCCGGGTGATCTTTTACTCGCCCAAGAT	1190
Db	841	TTCAACGAGGACACGGTGGCTGACATGACCCGGGTGATCTTTTACTCGCCCAAGAT	900
Qy	1191	GCCTGTGGAGTGTGACCTCCATGAATCTGGCATGCTTATGCGGACATGAACCTGAG	1250
Db	901	GCCTGTGGAGTGTGACCTCCATGAATCTGGCATGCTTATGCGGACATGAACCTGAG	960
Qy	1251	AATGTGCTTGTGATGACTGCGGACATCGAGAGTTATCTGACCTGGGAGCTGGAG	1310
Db	961	AATGTGCTTGTGATGACTGCGGACATCGAGAGTTATCTGACCTGGGAGCTGGAG	1020
Qy	1311	ATGAAGGGTGGCAAGCCCATCAACCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG	1370
Db	1021	ATGAAGGGTGGCAAGCCCATCAACCAGAGGGCTGGAACCAATGGTTACATGGCTCTGAG	1080
Qy	1371	ATCCTATGAAAAGGTAAGTATTTCTATCTGTGACCTGGTTTGCATGGGATGCAAC	1430
Db	1081	ATCCTATGAAAAGGTAAGTATTTCTATCTGTGACCTGGTTTGCATGGGATGCAAC	1140
Qy	1431	ATTATGAATGTTGTGCTGACGAACACACTTAAAGATTACAAGAAAAGGTCAGTAA	1490
Db	1141	ATTATGAATGTTGTGCTGACGAACACACTTAAAGATTACAAGAAAAGGTCAGTAA	1200
Qy	1491	GAGATCTGAAGCAAAAGACTCTGCAAGAGAGGTCAATTTCCAGCATGATTACTTACA	1550
Db	1201	GAGATCTGAAGCAAAAGACTCTGCAAGAGAGGTCAATTTCCAGCATGATTACTTACA	1260
Qy	1551	GAGAGCAAAAAGATTTTGGCAGGCTCTTCTTGGCTTAAGAAAACAAGCAACGCTTAA	1610
Db	1261	GAGAGCAAAAAGATTTTGGCAGGCTCTTCTTGGCTTAAGAAAACAAGCAACGCTTAA	1320
Qy	1611	AGCAGAAAAAGTGTGATGATCCCAAGAAACATCTTTTAAAGAAAGATCACTTCTCT	1670
Db	1321	AGCAGAAAAAGTGTGATGATCCCAAGAAACATCTTTTAAAGAAAGATCACTTCTCT	1380
Qy	1671	CGCTGGAAGCTGGCTAATTGAACCCCACTTGTGCGAGACCTTCAGTGGTTATGCTC	1730
Db	1381	CGCTGGAAGCTGGCTAATTGAACCCCACTTGTGCGAGACCTTCAGTGGTTATGCTC	1440
Qy	1731	AAAGACATCGCTGAATTTGATGATTTCTCTGAGGTTCTGGGGGTGGAAATTGATGACAA	1790
Db	1441	AAAGACATCGCTGAATTTGATGATTTCTCTGAGGTTCTGGGGGTGGAAATTGATGACAA	1500
Qy	1791	GATAGCAGCTTCTCAAAAACCTTGGACAGAGTCTGTCTATAGCATGCGCAGAGAA	1850

Db 1501 GATAGACAGTTCTTCAAAAACCTTGGCAGAGGTCGTCTTCTTACGATGGAGAGAA 1560
Qy 1851 ATTAGAAGCGGAGCTGTTGAGACATGATGACCCCAAGACCTTACGGGTTGAG 1910
Db 1561 ATTATGAAAGCGGAGCTGTTGAGAGATGATGACCCCAAGACCTTACGGGTTGAG 1620
Qy 1911 GAGGTAATTCATCCAGCTGCGGTGTGTTTATG 1949
Db 1621 GAGGTATTCATCCAGCTGCGGTGTGTTTATG 1659

RESULT 4
US-10-311-034-45

/ Sequence 45, Application US/10311034
/ Publication No. US20040023242A1
/ GENERAL INFORMATION:

/ APPLICANT: INCYTE GENOMICS, INC.
/ APPLICANT: YUE, Henry
/ APPLICANT: LAL, Preeti
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: BOROMSKY, Mark L.
/ APPLICANT: AU-YOUNG, Janice
/ APPLICANT: LU, Yan
/ APPLICANT: GANDHI, Ameena R.
/ APPLICANT: TRIBOLEY, Catherine M.
/ APPLICANT: CHAWLA, Nandinder K.
/ APPLICANT: VAO, Monique G.
/ APPLICANT: LU, Dying Alina M.
/ APPLICANT: GREENWALD, Sara R.
/ APPLICANT: RAMKUMAR, Jayalaxmi
/ APPLICANT: GRIFPIN, Jennifer A.
/ APPLICANT: KEARNEY, Liam
/ APPLICANT: BURBORD, Neil
/ APPLICANT: NGUYEN, Daniel B.
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: HE, Ann
/ APPLICANT: THORNTON, Michael
/ APPLICANT: HARELITA, April
/ APPLICANT: ARVIZU, Chandra S.
/ APPLICANT: GURURAJAN, Rajasopal
/ APPLICANT: LO, Terence P.
/ APPLICANT: KHAH, Farrah A.
/ APPLICANT: RECIPO, Shirley A.
/ APPLICANT: AZIMZAI, Yalda
/ APPLICANT: POLICKI, Jennifer L.
/ APPLICANT: DING, Li
/ APPLICANT: GREYHER, Megan
/ APPLICANT: ELLIOTT, Vicki S.
/ APPLICANT: THANGAVELU, Kavitha
/ APPLICANT: BATRA, Saivee
/ APPLICANT: ISON, Craig H.
/ TITLE OF INVENTION: HUMAN KINASES
/ FILE REFERENCE: PI-0125 PCT
/ CURRENT APPLICATION NUMBER: US/10/311,034
/ PRIOR FILING DATE: 2002-12-10
/ PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
/ 60/228,056
/ PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PERL Program
/ SEQ ID NO 45
/ LENGTH: 1662
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Query Match

75.5%; Score 1658.8; DB 17; Length 1662;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 291 ATGTGTGACATGGGGGCTTGGACAACTTATGTCACACCGCTTACCTGAGGCGCG 350
Db 1 ATGTGTGACATGGGGGCTTGGACAACTTATGTCACACCGCTTACCTGAGGCGCG 60
Qy 351 AAGCCCTCGACCTGACAGCAAGAGCTGCAAGCGCGCGCGCTTACCTGAGGCGCG 410
Db 61 AAGCCCTCGACCTGACAGCAAGAGCTGCAAGCGCGCGCGCTTACCTGAGGCGCG 120
Qy 411 GGGCTGACAGGCTGCGCGGAGCTCGCCAGAACTGTCCCTGAACTTCCAGCGCTGT 470
Db 121 GGGCTGACAGGCTGCGCGGAGCTCGCCAGAACTGTCCCTGAACTTCCAGCGCTGT 180
Qy 471 GAGCAGACGCCATCGGTGCGCGCTTTCCTGATCTTCTAGCAGAGTGCACGTTTC 530
Db 181 GAGCAGACGCCATCGGTGCGCGCTTTCCTGATCTTCTAGCAGAGTGCACGTTTC 240
Qy 531 CGCAAGGCGCAACCTTCTAGAGAGAGTGCAGAACTGGAGCTGGCCGAGAGGAGCC 590
Db 241 CGCAAGGCGCAACCTTCTAGAGAGAGTGCAGAACTGGAGCTGGCCGAGAGGAGCC 300
Qy 591 ACCAAGACAGCGCGCTGAGGCGCTGAGCCACTTGTGCGAGTGCCTGCGCGCG 650
Db 301 ACCAAGACAGCGCGCTGAGGCGCTGAGCCACTTGTGCGAGTGCCTGCGCGCG 360
Qy 651 AACCCGCAACCTTCTGACGAGCGCGTGGCCACCAAGTGCAGACCACTGAG 710
Db 361 AACCCGCAACCTTCTGACGAGCGCGTGGCCACCAAGTGCAGACCACTGAG 420
Qy 711 GAGAGGAGGTGCTGACGAGTGCAGGCTGAGGCTGAGGCTTCTTGGAAAG 770
Db 421 GAGAGGAGGTGCTGACGAGTGCAGGCTGAGGCTGAGGCTTCTTGGAAAG 480
Qy 771 CAGCCCTTAAAGATTTGTGACCAAGCGCTTACGACCAAGTTTGTGAGTGAATC 830
Db 481 CAGCCCTTAAAGATTTGTGACCAAGCGCTTACGACCAAGTTTGTGAGTGAATC 540
Qy 831 TTGAGATGCAACGAGTGTGACCAAGTACTTCACTGAGTTCAGAGTGTGAGAAAGT 890
Db 541 TTGAGATGCAACGAGTGTGACCAAGTACTTCACTGAGTTCAGAGTGTGAGAAAGT 600
Qy 891 GATTGTGGGAGATATGTCGCTGAGGAGGAGAAAGCTGGAGATGTATGCTGTAG 950
Db 601 GATTGTGGGAGATATGTCGCTGAGGAGGAGAAAGCTGGAGATGTATGCTGTAG 660
Qy 951 AAACCTGACAGAGCGGCTGAGAGAAAGTGGAGAGTGGCTGTGGAGAAAG 1010
Db 661 AAACCTGACAGAGCGGCTGAGAGAAAGTGGAGAGTGGCTGTGGAGAAAG 720
Qy 1011 GAAATCTTGGAGAGTGTGACAGCCCTTTCATTTCTCTGTGGCTATGCTTGGAGAC 1070
Db 721 GAAATCTTGGAGAGTGTGACAGCCCTTTCATTTCTCTGTGGCTATGCTTGGAGAC 780
Qy 1071 AAGACCAATCTGCTGCTGATGAGCTGATGATGATGATGATGATGATGATGATGATG 1130
Db 781 AAGACCAATCTGCTGCTGATGAGCTGATGATGATGATGATGATGATGATGATGATG 840
Qy 1131 TACAGGTGAGCAGCGCTGAGCAGTGAAGCGGAGTGTATCTTACTGAGCGCAGATA 1190
Db 841 TACAGGTGAGCAGCGCTGAGCAGTGAAGCGGAGTGTATCTTACTGAGCGCAGATA 900
Qy 1191 GCGTGTGAGAGTGTGACCTTCATTAAGTGGAGTGTATGATGAGAGCTGAG 1250
Db 901 GCGTGTGAGAGTGTGACCTTCATTAAGTGGAGTGTATGATGAGAGCTGAG 960
Qy 1251 AATGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1310
Db 961 AATGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1311 ATGAAGGCTGAGAGCGCATCAAGAGGCTGAGAACCAAGTGTATGATGCTGCTAG 1370

Db 1021 ATGAAGGTGGCAAGCCATCAACCAAGAGGCTGGAAACCATGTTATACATGCTCTCGAG 1080
 Oy 1371 ATCCAAATGAAAAAGTAAGTATTTCTATCTGTGAGCTGTTGCCATGGATGAC 1430
 Db 1081 ATCTTAATGAAAAAGTAAGTATTTCTATCTGTGAGCTGTTGCCATGGATGAC 1140
 Oy 1431 ATTTATGAATGTTCTGTGAGCAACACCTTCTAAAGTTTCAAGAAAAAGTCACTAA 1490
 Db 1141 ATTTATGAATGTTCTGTGAGCAACACCTTCTAAAGTTTCAAGAAAAAGTCACTAA 1200
 Oy 1491 GAGATCTGAAGCAAGAACTCTGCAAGAGAGTCAATTCAGCATGATTAATCTTCA 1550
 Db 1201 GAGATCTGAAGCAAGAACTCTGCAAGAGAGTCAATTCAGCATGATTAATCTTCA 1260
 Oy 1551 GAGAGCAAGAAAGTATTTGCAAGGCTCTTCTGCTAAGAAACAGAGCAAGCTTTAGA 1610
 Db 1261 GAGAGCAAGAAAGTATTTGCAAGGCTCTTCTGCTAAGAAACAGAGCAAGCTTTAGA 1320
 Oy 1611 ACCAGAGAAAGTCTGATGATCTCCAGAAACATCATTTCTTTAAAGATCAACTTCTCT 1670
 Db 1321 ACCAGAGAAAGTCTGATGATCTCCAGAAACATCATTTCTTTAAAGATCAACTTCTCT 1380
 Oy 1671 CGCTGGAAGCTGCGCTAATTAAGCCCATTTGTGCAAGCCCTTCAAGTGTATAGCC 1730
 Db 1381 CGCTGGAAGCTGCGCTAATTAAGCCCATTTGTGCAAGCCCTTCAAGTGTATAGCC 1440
 Oy 1731 AAAGACATGCTGAATTAATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAA 1790
 Db 1441 AAAGACATGCTGAATTAATGATTTCTCTGAGGTTGCGGGGTGGAATTTGATGACAA 1500
 Oy 1791 GATAGCAAGTCTTCAAAAACTTTGCGACAGGTCTGTTCCATAGCATGGCGAAGAA 1850
 Db 1501 GATAGCAAGTCTTCAAAAACTTTGCGACAGGTCTGTTCCATAGCATGGCGAAGAA 1560
 Oy 1851 ATTAATGAAGAGGAGCTGTTGAGACATGATGACCCCAAGACCTTACGCGTTGAG 1910
 Db 1561 ATTAATGAAGAGGAGCTGTTGAGACATGATGACCCCAAGACCTTACGCGTTGAG 1620
 Oy 1911 GAGGTATTCATCAAGTCTGCGTGTGTTGTTATTTGA 1952
 Db 1621 GAGGTATTCATCAAGTCTGCGTGTGTTGTTATTTGA 1662

RESULT 5

US-10-451-168-49
 ; Sequence 49, Application US/10451168
 ; Publication No. US20040091969A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION
 ; APPLICANT: SMITHKLINE BEECHAM P.L.C.
 ; APPLICANT: GLAXO GROUP LIMITED
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP50039
 ; CURRENT APPLICATION NUMBER: US/10/451,168
 ; CURRENT FILING DATE: 2003-11-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/49232
 ; PRIOR FILING DATE: 2000-12-17
 ; PRIOR APPLICATION NUMBER: 60/256,710
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,048
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 60/260,482
 ; PRIOR FILING DATE: 2001-01-09
 ; PRIOR APPLICATION NUMBER: 60/264,922
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/266,797
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/276,988
 ; PRIOR FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 60/281,535
 ; PRIOR FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: 60/289,622
 ; PRIOR FILING DATE: 2002-06-28

; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 49
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-451-168-49
 Query Match 75.5%; Score 1658.8; DB 17; Length 1662;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 291 ATGATGACATGAGGAGGCTCTGCAACAACTGATCCGCAACCGCTTACCTGAGAGCCCGG 350
 Db 1 ATGATGACATGAGGAGGCTCTGCAACAACTGATCCGCAACCGCTTACCTGAGAGCCCGG 60
 Oy 351 AAGCCCTCGGACCTGCAACAGAAAGCTGCAAGGCGGCGGCGGTAGGCTGAGCCCTGCC 410
 Db 61 AAGCCCTCGGACCTGCAACAGAAAGCTGCAAGGCGGCGGCGGTAGGCTGAGCCCTGCC 120
 Oy 411 GAGCTCAGAGGCTGCGGAGCTCCGCAAGAACTGTCTCTGAACTTCCACAGCCTGTGT 470
 Db 121 GAGCTCAGAGGCTGCGGAGCTCCGCAAGAACTGTCTCTGAACTTCCACAGCCTGTGT 180
 Oy 471 GAGCAGAGCCATATGCTGCGCCCTCTTCCGTGACTTCTTACGCAAGTCCAGCTTC 530
 Db 181 GAGCAGAGCCATATGCTGCGCCCTCTTCCGTGACTTCTTACGCAAGTCCAGCTTC 240
 Oy 531 CGCAAGCGGCAACCTTCTTGAAGAGAGCTGCAAGCTGAGCTGAGCGCAAGAGGACCC 590
 Db 241 CGCAAGCGGCAACCTTCTTGAAGAGAGCTGCAAGCTGAGCTGAGCGCAAGAGGACCC 300
 Oy 591 ACCAAAGACAGGCGCTGCAAGGAGCTGAGGCACTTGTGAGTCCCTGCGCGCGG 650
 Db 301 ACCAAAGACAGGCGCTGCAAGGAGCTGAGGCACTTGTGAGTCCCTGCGCGCGG 360
 Oy 651 AACCCGCAACCTTCTTCAAGCAGGCGGTGCGCAAGAGTCCCAAGAGCAGCACTAG 710
 Db 361 AACCCGCAACCTTCTTCAAGCAGGCGGTGCGCAAGAGTCCCAAGAGCAGCACTAG 420
 Oy 711 GAAAGAGAGTGGCTGCAAGTACCTCCGCAAGGCTGAGGCGCAATGCTTCTTGAAG 770
 Db 421 GAAAGAGAGTGGCTGCAAGTACCTCCGCAAGGCTGAGGCGCAATGCTTCTTGAAG 480
 Oy 771 CAGCCCTTAAGGATTTCTGACCAAGCGCTTCTTACCAAGATTTCTGAGTGAATCT 830
 Db 481 CAGCCCTTAAGGATTTCTGACCAAGCGCTTCTTACCAAGATTTCTGAGTGAATCT 540
 Oy 831 TTGAGATGCAACCAAGTCAAGCAAGTACTTCACTGAGTCAAGTGTGCGGAGAAAGT 890
 Db 541 TTGAGATGCAACCAAGTCAAGCAAGTACTTCACTGAGTCAAGTGTGCGGAGAAAGT 600
 Oy 891 GGTGTTGGGAGGATGTCGCTCAAGGTAAACACTGGAAGATGATGCTGTAG 950
 Db 601 GGTGTTGGGAGGATGTCGCTCAAGGTAAACACTGGAAGATGATGCTGTAG 660
 Oy 951 AAATCGCAAGAAAGCGCTGAAAGAAAGTGTGAGAGATGCTCTTGGAAAG 1010
 Db 661 AAATCGCAAGAAAGCGCTGAAAGAAAGTGTGAGAGATGCTCTTGGAAAG 720
 Oy 1011 GAAATCTGGAAGAGTCAAGAGCCTTTCATTTGTCTCTGCTTGTGAGAGC 1070
 Db 721 GAAATCTGGAAGAGTCAAGAGCCTTTCATTTGTCTCTGCTTGTGAGAGC 780
 Oy 1071 AAGACCATCTCTGCTGTCATGAGCTGATGAGTGAATGAGGAGAGCTTCAAGTTCACATC 1130
 Db 781 AAGACCATCTCTGCTGTCATGAGCTGATGAGTGAATGAGGAGAGCTTCAAGTTCACATC 840
 Oy 1131 TACAACTGAGGAGCGCTGAGCTGCAATGAGCCGAGTATTTTACTGCGCCGAGATA 1190
 Db 841 TACAACTGAGGAGCGCTGAGCTGCAATGAGCCGAGTATTTTACTGCGCCGAGATA 900
 Oy 1191 GCCTGTGGAGTGTGACCTCCATGAACTGCGGATGCTATCGGAGCATGAAGCTTGAG 1250

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Db      901  GCGTGGGATGCTGCACTTCACATGAACTCGGCAACGCTCATGCGGACATGAGCTCGAG 960
Qy      1251  AATGTCCTTCTGGAATGACCTTCGCACTCGAGTTATCTGACCTGCGGCTGCGCTGAG 1310
Db      961  AATGTCCTTCTGGAATGACCTTCGCACTCGAGTTATCTGACCTGCGGCTGCGCTGAG 1020
Qy      1311  ATGAAGGCTGCGCAACCCATCACCAGAGGCTGGAACCAATGTTATCATAGCTCTGAG 1370
Db      1021  ATGAAGGCTGCGCAACCCATCACCAGAGGCTGGAACCAATGTTATCATAGCTCTGAG 1080
Qy      1371  ATCTTATGAAAAGGTAAGTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 1430
Db      1081  ATCTTATGAAAAGGTAAGTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 1140
Qy      1431  ATTTATGAAAAGGTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 1490
Db      1141  ATTTATGAAAAGGTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 1200
Qy      1491  GAGATCTGAGCAAAAGCTGCGAAGCAAGCTCAATTCAGCATGATTAATCTTACA 1550
Db      1201  GAGATCTGAGCAAAAGCTGCGAAGCAAGCTCAATTCAGCATGATTAATCTTACA 1260
Qy      1551  GAGAAAGCAAAAGATATTGCAAGCTCTTCTGCTTATGAAACAGAGCAAGCTTATG 1610
Db      1261  GAGAAAGCAAAAGATATTGCAAGCTCTTCTGCTTATGAAACAGAGCAAGCTTATG 1320
Qy      1611  AGCAGAAAAGGTTGATGATCCGAGAAACATCATTTCTTAAACAGATCACTTCT 1670
Db      1321  AGCAGAAAAGGTTGATGATCCGAGAAACATCATTTCTTAAACAGATCACTTCT 1380
Qy      1671  CGCTGGAAGCTGCGCAATTAAGAACCCCAATTTGCGCAAGCTTATGATGTTATCC 1730
Db      1381  CGCTGGAAGCTGCGCAATTAAGAACCCCAATTTGCGCAAGCTTATGATGTTATCC 1440
Qy      1731  AAGAATCGCTGCAAAATGATGATTTCTGAGGTTGCGGAGGTTGAAATTTGATGAA 1790
Db      1441  AAGAATCGCTGCAAAATGATGATTTCTGAGGTTGCGGAGGTTGAAATTTGATGAA 1500
Qy      1791  GATTAAGCACTTCTTCAAAAATCTTGCAAGGCTGCTTCTTATGATGATGCAAGAA 1850
Db      1501  GATTAAGCACTTCTTCAAAAATCTTGCAAGGCTGCTTCTTATGATGATGCAAGAA 1560
Qy      1851  ATTATGAAGCGGGAATGTTGAGGAATGATGATGATGATGATGATGATGATGATGAT 1910
Db      1561  ATTATGAAGCGGGAATGTTGAGGAATGATGATGATGATGATGATGATGATGATGAT 1620
Qy      1911  GAGGTAATTCATCAAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1952
Db      1621  GAGGTAATTCATCAAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1662

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RESULT 6
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilgowski, Nathaniel L.
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA

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; ORGANISM: homo sapiens
US-10-217-745-1
Query Match      75.5%; Score 1658.4; DB 15; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      291  ATGTGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 350
Db      1  ATGTGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Qy      351  AAGGCTGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
Db      61  AAGGCTGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Qy      411  GGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 470
Db      121  GGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Qy      471  GAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 530
Db      181  GAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy      531  CGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 590
Db      241  CGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Qy      591  ACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 650
Db      301  ACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy      651  AACCCGCAACCCCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 710
Db      361  AACCCGCAACCCCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy      711  GAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 770
Db      421  GAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Qy      771  CAGCCTTTAAGATTTTGTGACAGAGGCTTCTGAGCAAGTTTCTGAGTGGAAATC 830
Db      481  CAGCCTTTAAGATTTTGTGACAGAGGCTTCTGAGCAAGTTTCTGAGTGGAAATC 540
Qy      831  TTGAGATGCAACAGATGTCAGCAAGATTTCTGAGTGGAAATTTCTGAGTGGAAAT 890
Db      541  TTGAGATGCAACAGATGTCAGCAAGATTTCTGAGTGGAAATTTCTGAGTGGAAAT 600
Qy      891  GGTGTTGGAGGAGGATGAGGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 950
Db      601  GGTGTTGGAGGAGGATGAGGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy      951  AAGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1010
Db      661  AAGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Qy      1011  GAAATCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1070
Db      721  GAAATCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy      1071  AAGACCATCTTCTGCTTGTATGAGGCTGATGATGATGATGATGATGATGATGATGAT 1130
Db      781  AAGACCATCTTCTGCTTGTATGAGGCTGATGATGATGATGATGATGATGATGATGAT 840
Qy      1131  TAAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
Db      841  TAAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy      1191  GCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1250
Db      901  GCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy      1251  AATGTCTTCTGATGACCTGCGCACTGAGGTTATCTGACCTGAGGCTGAGCTGAGG 1310

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Db 961 AATGCTCTGTGATGACCTGCGAACCTCAGATTATCTAAGCTGGGGCTGGCGTGGAG 1020
 Qy 1311 ATGAAGGTGCGAACCCCATCAACCGAGGCTGGAACCAATGTTATACATGCTCTGAG 1370
 Db 1021 ATGAAGGTGCGAACCCCATCAACCGAGGCTGGAACCAATGTTATACATGCTCTGAG 1080
 Qy 1371 ATCTTAATGGAAGGTAATTTCTTATCTCTGAGCTGTTTCCATGGAATGAGC 1430
 Db 1081 ATCTTAATGGAAGGTAATTTCTTATCTCTGAGCTGTTTCCATGGAATGAGC 1140
 Qy 1431 ATTTATGAATGTTTCTGAGCAACCAATTCATAAGATTAACAAGAAAGTCACTAA 1490
 Db 1141 ATTTATGAATGTTTCTGAGCAACCAATTCATAAGATTAACAAGAAAGTCACTAA 1200
 Qy 1491 GAGATCTGAAGCAAGAACTGCAAGACGAGTCAATTCAGATGATTAATCTTCA 1550
 Db 1201 GAGATCTGAAGCAAGAACTGCAAGACGAGTCAATTCAGATGATTAATCTTCA 1260
 Qy 1551 GAGAAAGCAAAAGATTTTTCAGGCTCTTCTGCTAAGAAACCAAGCAAGCTTGA 1610
 Db 1261 GAGAAAGCAAAAGATTTTTCAGGCTCTTCTGCTAAGAAACCAAGCAAGCTTGA 1320
 Qy 1611 ACAGAGAAAGTCTGATGATCCAGAAACATCAATTTCTTAAACGATCAATCTTCT 1670
 Db 1321 ACAGAGAAAGTCTGATGATCCAGAAACATCAATTTCTTAAACGATCAATCTTCT 1380
 Qy 1671 GCGCTGAGGCTGCTAATTTGAACCCCATTTGTCAGACCCCTTCAAGTGTATGCC 1730
 Db 1381 GCGCTGAGGCTGCTAATTTGAACCCCATTTGTCAGACCCCTTCAAGTGTATGCC 1440
 Qy 1731 AAAGCATCGCTGAATTTGATGATTTCTGAGGTTGGGGGGTGGAAATTTGATGACAA 1790
 Db 1441 AAAGCATCGCTGAATTTGATGATTTCTGAGGTTGGGGGGTGGAAATTTGATGACAA 1500
 Qy 1791 GATAAGCAGTTCTTCAAAAACCTTGGCAAGGCTGTTCTTATGAGATGCGAGAAAG 1850
 Db 1501 GATAAGCAGTTCTTCAAAAACCTTGGCAAGGCTGTTCTTATGAGATGCGAGAAAG 1560
 Qy 1851 ATTATAGAAACGGGACTGTTGAGGACTGATGACCCCAACAGACTGAGGTTGTAG 1910
 Db 1561 ATTATAGAAACGGGACTGTTGAGGACTGATGACCCCAACAGACTGAGGTTGTAG 1620
 Qy 1911 GAGGTAATTCATCAAGTCTGAGCTGTTGTTATGTAA 1952
 Db 1621 GAGGTAATTCATCAAGTCTGAGCTGTTGTTATGTAA 1662

RESULT 7
 US-09-964-469-1
 ; Sequence 1, Application US/09964469
 ; Patent No. US2002034803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PASTESEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-964-469-1
 Query Match 75.4%; Score 1657.2; DB 9; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 291 ATGTGACATATGGGGGCTCTGACCACTGATGCGCAACCGCTTACCTGAGGCTCCG 350
 Db 1 ATGTGACATATGGGGGCTCTGACCACTGATGCGCAACCGCTTACCTGAGGCTCCG 60
 Qy 351 AAGCCCTGCACTGCAAGCAAGAAAGCTGAGGCGGCGGCTGAGCTGAGCTGCTCC 410
 Db 61 AAGCCCTGCACTGCAAGCAAGAAAGCTGAGGCGGCGGCTGAGCTGAGCTGCTCC 120
 Qy 411 GGGCTGCAAGGCTGCGGAGAGCTCCGCAAGAGCTGCTGAACTTCAAGCTGTGT 470
 Db 121 GGGCTGCAAGGCTGCGGAGAGCTCCGCAAGAGCTGCTTAACTTCAAGCTGTGT 180
 Qy 471 GAGCAGAGCCCATCGGTGCGGCTCTTCCGTGACTTCTTACCAAGTCCACGTTTC 530
 Db 181 GAGCAGAGCCCATCGGTGCGGCTCTTCCGTGACTTCTTACCAAGTCCACGTTTC 240
 Qy 531 GCGAAGCGGCAACCTTCTTAAAGAGCTGCAAGCTGGAAGCTGGCTGAGAGGAGCC 590
 Db 241 GCGAAGCGGCAACCTTCTTAAAGAGCTGCAAGCTGGAAGCTGGCTGAGAGGAGCC 300
 Qy 591 ACCAAGACAGCGGCTGCAAGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 650
 Db 301 ACCAAGACAGCGGCTGCAAGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 360
 Qy 651 AACCGGCAACCTTCTTCAAGCAGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 710
 Db 361 AACCGGCAACCTTCTTCAAGCAGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 420
 Qy 711 GAAAGCAGTGGCTGCAAGCTGCGCAAGGCTGAGGCTGAGGCTTCTTTCGAAAG 770
 Db 421 GAAAGCAGTGGCTGCAAGCTGCGCAAGGCTGAGGCTGAGGCTTCTTTCGAAAG 480
 Qy 771 CAGCCCTTAAAGATTTGATGATGCAAGCGCTTCTTAAAGATTTCTGAGTAACTC 830
 Db 481 CAGCCCTTAAAGATTTGATGATGCAAGCGCTTCTTAAAGATTTCTGAGTAACTC 540
 Qy 831 TTGAGATGCAACAGTGTGCAAGAGTCTTCACTGATGTTGAGTGTGAGGAAAGT 890
 Db 541 TTGAGATGCAACAGTGTGCAAGAGTCTTCACTGATGTTGAGTGTGAGGAAAGT 600
 Qy 891 GATTTTGGGAGATATGTCGCTGCAAGTGAAGAACTGGAAGATTTGATGAGTAA 950
 Db 601 GATTTTGGGAGATATGTCGCTGCAAGTGAAGAACTGGAAGATTTGATGAGTAA 660
 Qy 951 AAATCTGACAAAGCGGCTGAAAGAAAGTGGCGAGAAAGTGGCTCTTGGAAAG 1010
 Db 661 AAATCTGACAAAGCGGCTGAAAGAAAGTGGCGAGAAAGTGGCTCTTGGAAAG 720
 Qy 1011 GAAATCTTGAAGAGTGAAGAGCCCTTCACTTGTCTCTGAGCTATGCTTGAAGC 1070
 Db 721 GAAATCTTGAAGAGTGAAGAGCCCTTCACTTGTCTCTGAGCTATGCTTGAAGC 780
 Qy 1071 AAGACCATCTGCTGCTGCTGATGATGAGCTGATGATGAGGAGGCTCAAGTTCACATC 1130
 Db 781 AAGACCATCTGCTGCTGCTGATGATGAGCTGATGATGAGGAGGCTCAAGTTCACATC 840
 Qy 1131 TCAACGTGGGCAAGGCGGCTGCAAGATGAGGCGGCTGATGATGAGGCGGCAATA 1190
 Db 841 TCAACGTGGGCAAGGCGGCTGCAAGATGAGGCGGCTGATGATGAGGCGGCAATA 900
 Qy 1191 GCGTGGAGATGCTGACCTTCAAGAACTGGAGTGTATGCGGAGCATGAAGCTTGA 1250
 Db 901 GCGTGGAGATGCTGACCTTCAAGAACTGGAGTGTATGCGGAGCATGAAGCTTGA 960
 Qy 1251 AATGCTTCTGATGATGATGCTGCAAGCTGCAAGGTTATCTGAGCTGGGCTGGCGTGA 1310
 Db 961 AATGCTTCTGATGATGATGCTGCAAGCTGCAAGGTTATCTGAGCTGGGCTGGCGTGA 1020
 Qy 1311 ATGAAGGTGCAAGGCGCATCAACCAAGGCTGGAACCAATGTTATCAAGCTCTGAG 1370
 Db 1021 ATGAAGGTGCAAGGCGCATCAACCAAGGCTGGAACCAATGTTATCAAGCTCTGAG 1080

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RESULT 8
US-10-425-962-1
? Sequence 1, Application US/10425962
? Publication No. US20030180786A1
? GENERAL INFORMATION:
? APPLICANT: GUEBSTER, Karl et al
? TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
? TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
? FILE REFERENCE: CL000636D1V2
? CURRENT APPLICATION NUMBER: US/10/425,962
? CURRENT FILING DATE: 2003-04-30
? PRIOR APPLICATION NUMBER: 09/964,469
? PRIOR FILING DATE: 2001-09-28
? PRIOR APPLICATION NUMBER: 09/738,894
? PRIOR FILING DATE: 2000-12-18
? PRIOR APPLICATION NUMBER: 60/208,331
? PRIOR FILING DATE: 2000-06-01
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 1662
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-425-962-1

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Query Match	75.4%	Score 1657.2	DB 15	Length 1662
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1659	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY 291 ATGTGGACATGGGGCCCTGGAGACACCTGATGCCAACCCGCTTAACCTGAGAGCCGG 350

Db 1 ATGTGTGACATGGGGGCGCCCTTGAGAACCTTGATGGCAACATCGCTTCACTTCGACGGCCGG 60

QY 351 AAGCCTTGGAATCGGACAGCAAAAGACTGACAGCGGCGGCGGCTGAGCCCTGGCC 410

Db 61 AAGCCTTGGAATCGGACAGCAAAAGACTGACAGCGGCGGCGGCTGAGCCCTGGCC 120

QY 411 GGGCTGGAAGGGCTGGCGGGAAGCTTCGCGAAGACTGCTCCGAACTTTCACAGCCCTGTGT 470

Db 121 GGGCTGGAAGGGCTGGCGGGAAGCTTCGCGAAGACTGCTCCGAACTTTCACAGCCCTGTGT 180

QY 471 GAGCAGAGAGCCCATGGGTGGCGGCTTCCTGACTTCCTGACCAAGCTGCCAGCTTC 530

Db 181 GAGCAGAGAGCCCATGGGTGGCGGCTTCCTGACTTCCTGACTTCCTGACCAAGCTGCCAGCTTC 240

QY 531 CGAAGCGGCAACCTTCTAGAGGACAGTGGAGAACTGGGAGCGGCGGAGAGGAGAACCC 590

Db 241 CGAAGCGGCAACCTTCTAGAGGACAGTGGAGAACTGGGAGCGGCGGAGAGGAGAACCC 300

QY 591 ACCAAGACAGCGGCTGCAAGGGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCCGGG 650

Db 301 ACCAAGACAGCGGCTGCAAGGGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCCGGG 360

QY 651 AACCCGCAACCTTCTCAGCGAGCGGCGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCCGGG 710

Db 361 AACCCGCAACCTTCTCAGCGAGCGGCGGCTGGTGGCACTTGTGCAAGTGGCCCTGGCCCGGG 420

QY 711 GAAGAGCGAGTGGCTGCAAGTGGCAAGCTGCGAGGCTCAAGGCTTCTTTCAGAGAG 770

Db 421 GAAGAGCGAGTGGCTGCAAGTGGCAAGCTGCGAGGCTTTCAGAGTCTGGGAGAAAGGT 480

QY 771 CAACCTTTAAGAACTTGTGTGACCAAGCGCCCTTTCAGCAAGTTTCTGACAGTGAATCTC 830

Db 481 CAACCTTTAAGAACTTGTGTGACCAAGCGCCCTTTCAGCAAGTTTCTGACAGTGAATCTC 540

QY 831 TTGAGATGCAACCAAGTGTGACCAAGTCTTCACTGATTCAGAGTGTGGAGAAAGGT 890

Db 541 TTGAGATGCAACCAAGTGTGACCAAGTCTTCACTGATTCAGAGTGTGGAGAAAGGT 600

QY 891 GGTTTGGGGAAGTATGTGGCCCTGCAAGGTGAAAAACCTGGGAGAAAGTATGCTCTGAG 950

Db 601 GGTTTGGGGAAGTATGTGGCCCTGCAAGGTGAAAAACCTGGGAGAAAGTATGCTCTGAG 660

QY 951 AAACCTGACAAAGACCGGCTGGAAGAAAGAGTGGGAGAAAGATGCTCTTCTGGAAGAG 1010

Db 661 AAACCTGACAAAGACCGGCTGGAAGAAAGAGTGGGAGAAAGATGCTCTTCTGGAAGAG 720

QY 1011 GAATCTTGGGAAGAGTGAAGCGCCCTTCACTTGTCTCTCTGGCCCTATGCTTGGAGAC 1070

Db 721 GAATCTTGGGAAGAGTGAAGCGCCCTTCACTTGTCTCTCTGGCCCTATGCTTGGAGAC 780

QY 1071 AAGACCCATCTCTGCTTGTCTATGAGGCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130

Db 781 AAGACCCATCTCTGCTTGTCTATGAGGCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

QY 1131 TGCACGTGGGCAAGCGGTGGCTGGACATGAGCCGGGTGATCTTTTACTGGGCCAGATC 1190

Db 841 TGCACGTGGGCAAGCGGTGGCTGGACATGAGCCGGGTGATCTTTTACTGGGCCAGATC 900

QY 1191 GCGCTGGGAGTGTGACCTCCATGAACCTGGGATGTGTCTATCGGGAACATGAAGCCTGAG 1250

Db 901 GCGCTGGGAGTGTGACCTCCATGAACCTGGGATGTGTCTATCGGGAACATGAAGCCTGAG 960

QY 1251 AATGTGCTTGTGATGACTCGGCAACTGCAAGGTATATGACCTGGGGGCGGCGCTGGAG 1310

Db 961 AATGTGCTTGTGATGACTCGGCAACTGCAAGGTATATGACCTGGGGGCGGCGCTGGAG 1020

QY 1311 ATGAAGGGTGGCAAGCCCATCAACCAAGAGGCTGGAAACAAATGGTTACATGGCTCTGAG 1370

Db 1021 ATGAAGGGTGGCAAGCCCATCAACCAAGAGGCTGGAAACAAATGGTTACATGGCTCTGAG 1080

QY 1371 ATCTAATGGAAGAGTAAAGTTATCTCTATCTGTGACCTGTTTGCATGGGATGACG 1430

RESULT 9
US-10-072-012-273
Sequence 273, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Mutalidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Fortak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072, 012
CURRENT FILING DATE: 2002-01-31
PRIORITY APPLICATION NUMBER: 60/265, 102
PRIORITY FILING DATE: 2001-01-30

Query Match	74.6%;	Score 1640.8;	DB 13;	Length 1701;
Best Local Similarity	98.7%;	Pred. No. 0;		
Matches 1693;	Conservative	0;	Mismatches	21;
			Indels	3;

OY	273	TGAGCCCGTGTCTCAGCATGTGTGACATAGGGGGCCCTGGACAAACGTGATGGCAACACC	332
Db	1	TGAGCCCGCTGTCTCAGCATGTGTGACATAGGGGGCCCTGGACAAACGTGATGGCAACACC	60
OY	333	GCCTACCTGCAGAGCCCGGAAAGCCTTCGAGCTGGCGACACAAAGAGCTGCAAGCGCGCGG	392
Db	61	GCCTACCTGCAGAGCCCGGAAAGCCTTCGAGCTGGCGACACAAAGAGCTGCAAGCGCGCGG	120
OY	393	CGTAGCTGGCCCTGACCCGAGCTGCAAGGACTGGGGGAGACTCCGCGAAGAGTGTCCCTG	452
Db	121	CGTAGCTGGCCCTGACCCGAGCTGCAAGGACTGGGGGAGACTCCGCGAAGAGTGTCCCTG	180
OY	453	AACCTCCAGAGCCGTGTGTGAGCAGAGCCCATGAGTGGCGGCTCTTCCGTGACTTCTTA	512
Db	181	AACCTCCAGAGCCGTGTGTGAGCAGAGCCCATGAGTGGCGGCTCTTCCGTGACTTCTTA	240
OY	513	GGCACAAGTGCACAGTTCGCCAAGCGGCCCACTTCTTAAGAGACGTGGAGAACGGGAA	572
Db	241	GGCACAAGTGCACAGTTCGCCAAGCGGCCCACTTCTTAAGAGACGTGGAGAACGGGAA	300
OY	573	CTGAGCGAGGAGGGAGCCCAACAAAGACAGCGCGCTGACAGGAGGCTGTGTGCG	632
Db	301	CTGAGCGAGGAGGGAGCCCAACAAAGACAGCGCGCTGACAGGAGGCTGTGTGCG	360
OY	633	AGTGGCCTTGCCCGGGAAACCTGCAACCTTCCTGTAGCGAGGCGGTGGCCACCAAGTGC	692
Db	361	AGTGGCCTTGCCCGGGAAACCTGCAACCTTCCTGTAGCGAGGCGGTGGCGACCAAGTGC	420
OY	693	CAAGCAGCCACACTGAGGAAAGCGAGTGGCTGCAAGTGAAGCTGGCGAAAGCTGAGGCC	752
Db	421	CAAGCAGCCACACTGAGGAAAGCGAGTGGCTGCAAGTGAAGCTGGCGAAAGCTGAGGCC	480
OY	753	ATGAGCTTTCCTTGAGAGAGCAAGCCTTTAAAGATTGTGTACAGAGGCGCTTACAGACAAG	812
Db	481	ATGAGCTTTCCTTGAGAGAGCAAGCCTTTAAAGATTGTGTACAGAGGCGCTTACAGACAAG	540
OY	813	TTTCTGCAAGTGGAACTCTTGAGATGCAACAGTGTCAAGACAGTACTTCACTAGATTC	872
Db	541	TTTCTGCAAGTGGAACTCTTGAGATGCAACAGTGTCAAGACAGTACTTCACTAGATTC	600
OY	873	AGAGTGTGGGAAAGGTGTGTTTGGGAGGTATGTCCGCTCAAGTGAATAAACCTGAG	932

Db 601 AGAGTCTGGGAGAAAGTGTGTTTGGGAGGTA-----AAAAACCTGGG 645
 QY 933 AAGATGATGCTCTGTATAGAACTGACAAAGAGCGGCTGAAGAAGAAAGTGGGAGAG 992
 Db 646 AAGATGATGCTCTGTATAGAACTGACAAAGAGCGGCTGAAGAAGAAAGTGGGAGAG 705
 QY 993 ATGCTCTCTTGGAAAAGAAATCTTGGAGAGTCAAGAGCCCTTCAATGTCCTG 1052
 Db 706 ATGCTCTCTTGGAAAAGAAATCTTGGAGAGTCAAGAGCCCTTCAATGTCCTG 765
 QY 1053 GCTATGCTCTTGGAGAGAGAGCCATCTCTGCTCTGTATGAGCTGATGATGAGGGA 1112
 Db 766 GCTATGCTCTTGGAGAGAGAGCCATCTCTGCTCTGTATGAGCTGATGATGAGGGA 825
 QY 1113 GACCTAATGCTCAATCTCAAGAGTGGGAGCGGCTGAGCATGAGCGGCTGATC 1172
 Db 826 GACCTAATGCTCAATCTCAAGAGTGGGAGCGGCTGAGCATGAGCGGCTGATC 885
 QY 1173 TTTTACTGCGCCAGATAGCTGTGGAGTGTGACCTCATGAACTGGGATGCTAT 1232
 Db 886 TTTTACTGCGCCAGATAGCTGTGGAGTGTGACCTCATGAACTGGGATGCTAT 945
 QY 1233 CGGGAATGATAGAGCTGAGATGTGCTTCTGATGACCTGCGCACTGAGGTTATCTGAC 1292
 Db 946 CGGGAATGATAGAGCTGAGATGTGCTTCTGATGACCTGCGCACTGAGGTTATCTGAC 1005
 QY 1293 CTGGGAGTGGGCTGAGATGAAAGGTTGGCAAGCCATACCCAGAG---GGCTGAACC 1349
 Db 1006 CTGGGAGTGGGCTGAGATGAAAGGTTGGCAAGCCATACCCAGAGCGGCTGGAACC 1065
 QY 1350 AATGCTTACATGCTCTGATGATCTTATGAGAAAGTAAAGTATTCCTTCTGCTGAGC 1409
 Db 1066 AATGCTTACATGCTCTGATGATCTTATGAGAAAGTAAAGTATTCCTTCTGCTGAGC 1125
 QY 1410 TGGTTTGCATGGGATGCACTTTATGAATGTTGCTGAGCAAGCAACCTTCAAAAT 1469
 Db 1126 TGGTTTGCATGGGATGCACTTTATGAATGTTGCTGAGCAACCTTCAAAAT 1185
 QY 1470 TACAGAGAAAGTCTGTAAGAGGATCTGAACAAAGATCTTGCAGAGCAAGGTGAA 1529
 Db 1186 TACAGAGAAAGTCTGTAAGAGGATCTGAACAAAGATCTTGCAGAGCAAGGTGAA 1245
 QY 1530 TTCCAGCATGATTAATCTTCAAGAGAGCAAAAGATTTTCAGAGCTCTTCTGCTAAG 1589
 Db 1246 TTCCAGCATGATTAATCTTCAAGAGAGCAAAAGATTTTCAGAGCTCTTCTGCTAAG 1305
 QY 1590 AACCCAGAGCAAGCTTGAAGC---AGAGAAAGTCTGATGATCCAGAGAAATCAT 1646
 Db 1306 AACCCAGAGCAAGCTTGAAGAGAGAGAGAAAGTCTGATGATCCAGAGAAATCAT 1365
 QY 1647 TTCTTAAACGATCACTTCTGCTGCTGAGAGCTGAGCTAATGACCCCATTTGTG 1706
 Db 1366 TTCTTAAACGATCACTTCTGCTGCTGAGAGCTGAGCTAATGACCCCATTTGTG 1425
 QY 1707 CCAAGCTTCAAGTGTATGATCCAAAGACATGCTGAATATGATATTCCTGAGAGT 1766
 Db 1426 CCAAGCTTCAAGTGTATGATCCAAAGACATGCTGAATATGATATTCCTGAGAGT 1485
 QY 1767 CGGAGGCTGAGATTTGATGACAAAGTAAAGCATTTTCAAAAATTGCGACAGGTGCT 1826
 Db 1486 CGGAGGCTGAGATTTGATGACAAAGTAAAGCATTTTCAAAAATTGCGACAGGTGCT 1545
 QY 1827 GTTCTTATGATGAGAGAGAAATTAAGAAAGCGGATGTTTGAAGAACTGATGAC 1886
 Db 1546 GTTCTTATGATGAGAGAGAAATTAAGAAAGCGGATGTTTGAAGAACTGATGAC 1605
 QY 1887 CCCAAGACCTTACAGGCTGTGAGAGGTAATTCATCAAGCTGAGGCTGCTGTTGTA 1946
 Db 1606 CCCAAGACCTTACAGGCTGTGAGAGGTAATTCATCAAGCTGAGGCTGCTGTTGTA 1665
 QY 1947 TTGTAATGCTCTCTTTACAGAGCAAGCAAGCAAGCA 1982
 Db 1666 TTGTAATGCTCTCTTTACAGAGCAAGCAAGCAAGCA 1701

RESULT 10
 US-10-217-745-3
 ; Sequence 3, Application US/10217745
 ; Publication No. US20030004328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
 ; TITLE OF INVENTION: Polynucleotides
 ; FILE REFERENCE: Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; PRIOR FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: US/09/802,117
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-217-745-3
 Query Match 47.6%; Score 1046.8; DB 15; Length 1062;
 Best Local Similarity 99.8%; Pred. No. 1.7e-308;
 Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 291 ATGTGATGATGAGGAGGCTGAGCAACCTGATTCGCAACCGCTTACCTGAGGCGG 350
 Db 1 ATGTGATGATGAGGAGGCTGAGCAACCTGATTCGCAACCGCTTACCTGAGGCGG 60
 QY 351 AAGCTTGTGATGAGCAACAGAAAGTGTGAGAGCGGCGGCGTGAAGCTGAGGCGG 410
 Db 61 AAGCTTGTGATGAGCAACAGAAAGTGTGAGAGCGGCGGCGTGAAGCTGAGGCGG 120
 QY 411 GAGCTGAGAGGCTGAGGAGCTCGGCAAGCTGTCCCTGAACTTCCAGAGCTGTGT 470
 Db 121 GAGCTGAGAGGCTGAGGAGCTCGGCAAGCTGTCCCTGAACTTCCAGAGCTGTGT 180
 QY 471 GAGAGCAAGCCATGAGTGGCGGCTTCCGCTGATCTTCTGAGCCAGTGTCCAGGTT 530
 Db 181 GAGAGCAAGCCATGAGTGGCGGCTTCCGCTGATCTTCTGAGCCAGTGTCCAGGTT 240
 QY 531 CGCAAGCGGCAACCTTCTAGAGAGCTGAGAACTGAGAGCTGAGAGAGGAGCC 590
 Db 241 CGCAAGCGGCAACCTTCTAGAGAGCTGAGAACTGAGAGCTGAGAGAGGAGCC 300
 QY 591 ACCAAGACAGCGGCTGAGAGGCTGTGACCTTGTGAGAGTGTGAGGCTGAGGAG 650
 Db 301 ACCAAGACAGCGGCTGAGAGGCTGTGAGAGTGTGAGAGTGTGAGGCTGAGGAG 360
 QY 651 AACCCGCAACCTTCTGAGAGAGCGGCTGAGAGCAAGTGTGAGAGCAAGCACTGAG 710
 Db 361 AACCCGCAACCTTCTGAGAGAGCGGCTGAGAGCAAGTGTGAGAGCAAGCACTGAG 420
 QY 711 GAGAGCAAGTGTGAGAGCAAGTGTGAGAGCAAGTGTGAGAGCAAGTGTGAGAG 770
 Db 421 GAGAGCAAGTGTGAGAGCAAGTGTGAGAGCAAGTGTGAGAGCAAGTGTGAGAG 480
 QY 771 GAGCCCTTAAAGATTTGATGACCAAGCGCTTCAAGCAAGTGTGAGAGCAAGT 830
 Db 481 GAGCCCTTAAAGATTTGATGACCAAGCGCTTCAAGCAAGTGTGAGAGCAAGT 540
 QY 831 TTGAGATGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGT 890
 Db 541 TTGAGATGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGTGTGAGCAAGT 600
 QY 891 GGTTTTGGAGAGTATGCGCTGCAAGTGTGAGAGCAAGTGTGAGAGTGTGAGAG 950
 Db 601 GGTTTTGGAGAGTATGCGCTGCAAGTGTGAGAGCAAGTGTGAGAGTGTGAGAG 660

539 CGACIACCCTGGACAGCATCTACTTCAACCGTTTCTCGAGTGGAAAGTGGCTGGAAAGGCG

Db	599	GCCAGTACCAAAAAACA	CTTCAGGCAATACCGAGTCTG	GGCAAGGTGGCTTTGGGGA	658
Qy	902	GGATATGGCCGCTCA	GGTGAAGAACTG	GGGAAGATATATGCTGTAAAGAACTGGACA	961
Db	659	GGTGTGGCTTCGAG	GGTGGCGGCGACAGAGTAA	GTATGTATGACCTCGAAGAACTGAGAA	718
Qy	962	GAACCGGCTGAAG	AAAAAGGTGGCA	GAATGGCTCTCTTGGAAAAAGAAATCTTTGGA	1021
Db	719	AAACCGGATCA	AGAAAGCGGAAAGCGGACCTG	AGCCCTAAACGAAAGCAGATCTCGGA	778
Qy	1022	GAAGTACAGAGCC	CTTTCATTTGCTCTG	AGCTATAGGCTTTGAGAGCAAGACCAATCT	1081
Db	779	GAAGTAAACG	AGAGTGTGTGATG	AGCTTGGCTTAGCCTTAGAGACCAAGACGGGCT	838
Qy	1082	CTGCTTTGATG	AGCTGATGAATGGGAGAGACCT	CAAGTTCCACATCTACAACTGTGG	1141
Db	839	GTGGCTGGTGTCA	CTGATGAAACGGGGGCGACCTCA	AGTTCCACATCTCAACATGGG	898
Qy	1142	CACGCTGGCCCTG	AGACATGACCGGGATCTTTTAC	TCGGCCCAAGATGCTGTGGAGAT	1201
Db	899	CCAGGCTGGCTT	CCCCGAAGCGGGGCGGTCTT	CTAGCGCGGAGATCTGTGTGGCT	958
Qy	1202	GCTGACCTGCAT	GAAGACTGGCATGCTATG	CTGGGACATGAGGCTGAGATGTGCTTCT	1261
Db	959	GGAGGACCTG	ACCGGAGACGATCGTGTAC	GGGACCTGAAAGCCGAGAACATCTTGCT	1018
Qy	1262	GGATGACCTCGG	CACTCGAGATTATCTG	ACCTGGGCGTGGCGCTGGAGATGAAAGGTGG	1321
Db	1019	GGATACCAAGG	CCACATCCGATCTG	ACCTGGGACCTGATGTGCCCGAGGG	1078
Qy	1322	CAAGCCATCA	CCCAAGAGGCTGGAAACCA	TGGTTACATGAGCTCTCGAGATCTCTATGGA	1381
Db	1079	CCAGACCTAT	CAAAAGGCGTGGAGCACCGG	GGTTACATGAGCTCTCGAG--GTGGTGA	1135
Qy	1382	AAAGGATGTTAT	CTCATCTCTG	TGAGACTGGTTTGCATGAGATGACAGATTTATGAAT	1441
Db	1136	GAATGACGTA	CACTGTTCAAGCCCTG	AGCTGGGCGCTCGCTCTCTGTAGAGAT	1195
Qy	1442	GGTGTGAGAA	CACCACTTCAAA	GATTTACAGAAAGGTCTAGTAAAGAGATCTGAA	1501
Db	1196	GATCAAGG	CAGCTGGCTTCCAC	ACAGAGAAAGAAAGATCAAGCGGAGAGAGTGG	1255
Qy	1502	GCAAGAC	CTCGAACAAGAGTCA	ATTCCAGCACTGATTAACCTTCACAGAGGAGAA	1561
Db	1256	GCGGCTGTGA	AGAGGTCCCGAGAGATTTCC	AGGAGTTCCTCCCGAAGGCCGCTC	1315
Qy	1562	AGATATTTG	CAGGCTCTTCTTGGCT	TAAGAAACAGAGCAACCTTAGAAGCAGAGAA	1621
Db	1316	ACTTTGCTCA	AGCTCTCTCGAAGAACCTG	CGGAAACCTCGGAGGTGTGTGTGGGGGAG	1375
Qy	1622	GTCTGATGAT	CCCGAAGAAATCATATTTCTTTAA	AGATCAATCTTCTCGCTCGGAGAGC	1681
Db	1376	TGCCCCGAG	GTGAGAGACCCCTCTTTAA	AGAGCTGAACCTTCAAGCGGCTGGAGAC	1435
Qy	1682	TGGGCTAAT	TGAACCCCATTTGTG	CAGACCTTCAGTGTTTATGTCCAAAGACATGCG	1741
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Qy	1742	TGAATTTG	ATGATTTCTCTAGGTT	CGGGGGTGGAAATTTGATGACAAAGTAAAGAGTT	1801
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Qy	1802	CTTCAAAA	CTTTGGGACAGGTGCTG	TTCTCTATGCACTGGCAGAGAAATTTATGAAC	1861
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Qy	1862	GGGAC	CTGTTGAGGA	ACTGATGAC	1886
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US-09-873-367C-142
; Sequence 142, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:

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1  APPLICANT: Soppet, Daniel
2  APPLICANT: Andress, Gregory
3  APPLICANT: Augustus, Meena
4  APPLICANT: Ebner, Reinhard
5  APPLICANT: Carter, Kenneth
6  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
7  TITLE OF INVENTION: Signature Gene Sets
8  FILE REFERENCE: 689290-64
9  CURRENT APPLICATION NUMBER: US/09/873.367C

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CURRENT FILING DATE: 2003-04-29
PRIORITY APPLICATION NUMBER: U.S. 60/236,891
PRIORITY FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: U.S. 60/236,842
PRIORITY FILING DATE: 2000-09-29
PRIORITY APPLICATION NUMBER: U.S. 60/244,867
PRIORITY FILING DATE: 2000-11-01
PRIORITY APPLICATION NUMBER: U.S. 60/245,084
PRIORITY FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-142

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Query Match 19.0%; Score 418.2; DB 10; Length 2848

Best Local Similarity	90.26%
Mismatches	890;
Conservative	0;
Mismatches	683;
Indels	12;
Gaps	5.

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65 GGACTCGAGACATCGTAGGCAACGCTGCTACTCAAGGCCGGGAAAGTGGCGGTGG 124

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Db 125 AAATCGCAAGCCAAAAGCAGAAATGGCGCGAGATGCTCCAGTTCCCTCAGCATCAGCCA 184

422 CTGCGCGAGCTCCGCGAGAAGTGTCCCTGAATTCCACAGCCGTGTGTGAGCAGCAGCC 481

Db 185 GTGCCAGAGCTGCGGCTCAGGCTCGAGCGTGACTATCAAGGCTGTGCGAGCGGCAAGC 244

482 CATCGTCCGGCCTCTTCGGACTTCCTAGCCACAGTGCACGTTCCGCAAGGCGGC 541

Db
245 CATTGGGCGCTGCTGTTCCGAGTTCGTGCCACGAGGCCGAGCTAGCCGCTGCGT 304

542 AACCTTCTAGAGAGACGTGCAGAACTGGAGCTGGCCGAGGAGGGACCCACCAAGACAG 601

305 CGCCTTCTGATGGGGTGGCCGATGTAAGTGA CCCC GGATGCAAGCGGAGGCATG 364

602 CGCGCTGCAAGGGCTGGTGGCCACTTGTGTGGAGTGGCCCCCTGCCCCGGGGAAACCCGCAACC 661

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db 422 GGTCCCGGCAAGCTGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCTGCAAG 480

722 GGCTGCAGTGAACCTGCCCAAGGTGAAGCCATGCTTCTTGCAGAGCAGCCCTTAA /81

Db 481 ACC¹TTTTCAGAACTACCCGGCTGA---CCCACAGTACTGAGCGTGGCCCTTTTGC 538

782 GGAATTGGTACCAAGCGGCTTCTACGACAAATTTCGACATGGGAACCTTCGAGANGCA 84

Db 539 CGACTACCTGCACGATCTACTTCAACCGTTTCTGCACTGGAAGTGGCTGGAAGGCA 599

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Db 599 GCCAGTACCAAAAAACCTTCAGGCATACGAGTCCCTGGCAAAAGGCTTTGGGGA 658
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 QY 962 GAAGCGCTGAAGAAAGGTGGCCAGAAAGTGGCTCTCTTGGAAAAAGAAATCTTGA 1021
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 QY 1022 GAAGGTACAGACCCCTTTCATGTCTCTCTGCTATGCTTGGAGACAGACCATCT 1081
 Db 779 GAAAGTGAACAGTAGTGTGTAGTAGCTTGGCCCTTAGCTTAGAGACAGAGCGGCT 838
 QY 1082 CTGCTTGTATGAGCGCTGTATGATGAGGAGAGACCTTAGCTTCACTTCAACGCTGGG 1141
 Db 839 GTGCTGTGTCTGACACTGATGAAACGGGAGGAGACCTTCAAGTTCACATCTACACATGGG 898
 QY 1142 CACGCTGCGCTGACATGAGCCGGGTATCTTTTACTGCGGCCAGATAGCTGTGGAT 1201
 Db 899 CAGGCTGCTTCCCCAAGCGCGGCGCTCTTCAAGCGCGGATCTGTGTGGCT 958
 QY 1202 GCTGACCTTCATGAACTCGGATCGTCTATCGGACATGAAAGCTGGAATGTGCTTCT 1261
 Db 959 GAGAGACCTGACCGGAGGCGCATCTGTACAGGAGACCTGAAGCCGAGAACTTGTCT 1018
 QY 1262 GATGACCTCGGCACTGAGGATTTCTGACTTGGGCTGGCTGGCTGAGATGAGGCTGG 1321
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 Db 1079 CAGACATTCAAAGGCGGTGTGGGACCGTGGGTATCATGTGTCTGGAG---GTGGTAA 1135
 QY 1382 AAAAGTAAATTTCTTATCTGTGATGCTGTTGGCATGGATGAGCATTTATGAAAT 1441
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 QY 1442 GGTGCTGAGACGAAACCACTTCAAGATTTCAAGAAAGGTCAAGTAAAGGATCTGAA 1501
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 Db 1256 GCGGCTGTGAAGAGTCCCGAGAGATTTCCAGGCTTTTCCCGAGGCGCGCT 1315
 QY 1562 AATATTTTGAAGCTCTTCTTGGCTAAAGAAACCAAGCAAGCTTGAAGAGAGAA 1621
 Db 1316 ACTTGTCTCAAGCTCTCTGCAAGAGACCTGCGAAGCGCTGGGGTGTCTGGGGGAG 1375
 QY 1622 GTGTGATGATCCAGAAACATCTTTTAAAGCATCACTTCTCTGCTGGAAGC 1681
 Db 1376 TGCCCCGAGGTGAAGAGACCCCCCTTTTAAAGCTGAATTCACAGGCTGGAGC 1435
 QY 1682 TGCGCTAATGAACCCCATTTTGGCAGACCTTCAGTGGTTTATGCGAAGACATGCG 1741
 Db 1436 TGGAATGCTGAGCGCGCTTCAAGCTTGAACCCCAAGCATTTTACGAGAGATGCT 1495
 QY 1742 TGAATTTGATGATTTCTTGAAGTTTGGGAGGTGGAATTTGATGAGAAAGATGAGCAT 1801
 Db 1496 GAGCATTTGAACAGTTCTTACGCTCAAGGGCGTGAAGCTGAACGACAGAGACTT 1555
 QY 1802 CTGAAAACTTTGGAGAGGTGTGTTCTTATGACATGCGAGAGAAATTTATGAAAC 1861
 Db 1556 CTACAGAGATTTGCAAGGCAAGTGTGCTTCCCTGGAGAAAGAGATGTGGAGAC 1615
 QY 1862 GAGACTGTTTGAAGAACTGAATGAC 1886
 Db 1616 CGAGTGTCTCAAGAGCTGAATGTC 1640

; Sequence 4, Application US/10159856
 ; Publication No. US20030228689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
 ; FILE REFERENCE: RTS-0365
 ; CURRENT APPLICATION NUMBER: US/10/159,856
 ; CURRENT FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 134
 ; SEQ ID NO 4
 ; LENGTH: 2848
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (63) ... (1793)
 ; US-10-159-856-4

Query Match 19.0%; Score 418.2; DB 16; Length 2848;
 Best Local Similarity 56.2%; Pred. No. 4.2e-116;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 305 GGCCTTGAACAACCTGATGCAACACCGCTTACCTGAGAGCCGGAAGCCCTGAGACTG 364
 Db 65 GAGCTTGAAGACATCTGAGGAAACGCTGTACTCAAGGCTTGAAGAGTGGCGGTGG 124
 QY 365 CGACAGCAAG---AGTGAAGCGCGCGGAGTGAAGCTTGGCCCTGCGGCTGAGAG 421
 Db 125 AATTCGAAAGGCAAAAGCAAAATGGCGGACATGCTCAAGTTCCTTCAATCAGCCA 184
 QY 422 CTGGGCGAGCTCCCGCAAGAGCTGTCTTCACTTCAACAGCTGTGTGAGCAGAGCC 481
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 QY 482 CATCGGTGCGCTCTTCTGCTGACTTCTTCAAGTCCAGAGTCCGAGGTTCCGAGAGGCG 541
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 QY 602 CGGCTGAGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
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 QY 782 GATTTTGTGACAGAGCGCTTCTGAGCAAGATTTTGTGAGTGAAGATCTTCAAGATGCA 841
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Db 779 GAAAGTGAACAGTAGGTTTGTAGTGAAGCTTGGCTTAAGCTTATGAGACCAAGAGAGGGCT 838
QY 1082 CTGCTTGTATGATGAGCTGTATGAATGAGGAGAGACTCAAGTTCCATCTACACAGTGGG 1141
Db 839 GTGCTGTGTCTGACCTGATGAAAGGAGGAGAGCTCAAGTTCCATCTACACAGTGGG 898
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Db 899 CAGGCTGTGCTTCCCGAAGGCGGGCCGCTTCTACGCGCGAGATCTGCTGTGGCT 958
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Db 1256 GCGGCTGTGAGAGAGTCCCGAGAGATTCGAGCGCTTTCCCGAGGCGGCTC 1315
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QY 1622 GTCTGATGATCCAGAGAAATCATCTTTTAAAGATCACTTCTGCTGAGAGC 1681
Db 1376 TGCCGCGAGGAGAGAGACCCCTCTTAAGAGCTGAATTCAGCGGCTGGGAGC 1435
QY 1682 TGAGCTAATTGAACCCCATTTGTGCGAGACCTTCAAGTGTGTTATGCCAAGACATGGC 1741
Db 1436 TGCGATGCTGAGCGCGCTTCAAGCTGACCCCAAGGCCATTTCAGAGAGATGTTCT 1495
QY 1742 TGAATTTGATTTCTCTGAGGTTCCGGGGGTGAAATTTGATGACAAAGATAGCAGTT 1801
Db 1496 GAGCATTTGAACGTTCTCTACGTTCAAGGGGCTGAGCTGAGCTTACCAACAGAGATT 1555
QY 1802 CTTCAAAACCTTTGCAAGAGTGTGCTTCTAATGATGAGAGAGAAATTAATGAAC 1861
Db 1556 CTACGAGAGTTTGCAAGAGGCTGAGTGTGCTTCCCTGCGAAGAGAGATGTGAGAC 1615
QY 1862 GCGACTGTTGAGAACTGAATGAC 1886
Db 1616 CGAGTCTTCAAGAGCTGAATGTC 1640

Search completed: August 13, 2004, 19:06:08
Job time : 698.966 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 12:57:35 ; Search time 3850.63 Seconds

(without alignments)
17045.794 Million cell updates/sec

Title: US-10-044-205a-1

Perfect score: 2198
Sequence: 1 gacctaagatgaaggacc.....aacactcagttatttga 2198

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_ply:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	398.6	18.1	2978	AK051405	AK051405 Mus muscu
2	376	17.1	2989	BC057206	BC057206 Mus muscu
3	311.8	14.2	1201	BX404586	BX404586 BX404586
4	311.6	14.2	2329	BC027597	BC027597 Homo sapi

C	5	307	14.0	917	13	EX392018	EX392018 BX392018
	6	304.6	13.9	1721	29	AY406080	AY406080 Homo sapi
	7	300.2	13.7	1058	13	BQ057469	BQ057469 AGENCOURT
	8	299.2	13.6	1019	13	BQ061148	BQ061148 AGENCOURT
	9	295	13.4	1721	29	AY406082	AY406082 Mus muscu
	10	281.8	12.8	934	13	BQ526699	BQ526699 AGENCOURT
	11	280.6	12.8	903	13	BUI46436	BUI46436 AGENCOURT
	12	272.2	12.4	560	12	BM794145	BM794145 K-EST0075
	13	272.2	12.4	601	12	BM697459	BM697459 UI-E-DX0-
	14	272.2	12.4	1017	13	BQ061150	BQ061150 AGENCOURT
C	15	270.6	12.3	815	9	AI934968	AI934968 wdl1a07.x
	16	269.6	12.2	900	13	BQ071614	BQ071614 AGENCOURT
	17	269.2	12.3	857	13	BQ527897	BQ527897 AGENCOURT
	18	268.8	12.2	968	13	BQ066445	BQ066445 AGENCOURT
	19	267	12.1	1028	13	BQ063841	BQ063841 AGENCOURT
C	20	265.6	12.1	696	10	BE677821	BE677821 AGENCOURT
	21	265.4	12.1	998	13	BQ057613	BQ057613 AGENCOURT
	22	264.8	12.0	1032	12	BM472080	BM472080 AGENCOURT
	23	264.4	12.0	1034	10	BE568334	BE568334 AGENCOURT
	24	264.2	12.0	851	13	BQ230423	BQ230423 AGENCOURT
	25	264.2	12.0	1622	29	AY406081	AY406081 Pan trogl
	26	263.6	12.0	826	12	BG828886	BG828886 602752869
	27	263	12.0	777	10	BE795217	BE795217 601592482
C	28	258	11.7	713	10	AM173009	AM173009 X182411.x
	29	258	11.7	1057	13	BQ071329	BQ071329 AGENCOURT
	30	256	11.6	543	10	BE394617	BE394617 601311853
	31	254.8	11.6	707	12	BQ823182	BQ823182 60276540
C	32	253.6	11.5	769	13	BM013848	BM013848 BM013848
	33	252.8	11.5	892	14	CB195631	CB195631 AGENCOURT
	34	252.4	11.5	838	13	BX849055	BX849055 BX849055
C	35	250.2	11.4	810	13	BM085647	BM085647 BM085647
	36	249	11.3	676	9	AI640213	AI640213 wa30e01.x
C	37	247.8	11.3	792	13	BX684426	BX684426 BX684426
	38	244.4	11.1	660	13	BQ520195	BQ520195 NTSC n103
	39	243.2	11.1	1351	13	BQ213536	BQ213536 AGENCOURT
	40	240.2	10.9	995	13	BQ056240	BQ056240 AGENCOURT
	41	239.4	10.9	569	12	BM712420	BM712420 UI-E-DWI-
C	42	239.4	10.9	658	9	AI738477	AI738477 w332d04.x
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ALIGNMENTS

RESULT 1
LOCUS AK051405
DEFINITION Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone: D130046K22 product: c PROTEIN-COUPLED RECEPTOR KINASE GPR6 (EC 2.7.1.1-) homolog [Mus musculus], full insert sequence.
ACCESSION AK051405
VERSION AK051405.1 GI:26094516
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Carinci, P., and Hayashizaki, Y.
Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
1 Carinci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

REFERENCE
1 Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shiota, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Preparation of full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
1 Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shiota, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Preparation of full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159
 SHIBAHARA, K., ITOH, M., AIZAWA, K., NAGAOKA, S., SASAKI, N., CARMINCI, P., KONO, H., AKIYAMA, Y., NISHI, K., KITSUMI, T., TASHIRO, H., ITOH, M., SUMI, N., ISHII, Y., NAKAMURA, S., HAZAMA, M., NISHINE, T., HARADA, A., YAMAMOTO, R., MATSUMOTO, H., SAKAGUCHI, S., IKEYAMA, T., KASHIWAGI, K., FUJIWAKE, S., INOUE, K., TOGAWA, T., IZAWA, M., OHARA, E., WATABIKI, M., YONEDA, Y., ISHIKAWA, T., OZAWA, K., TANAKA, T., MATSURA, S., KAWAI, J., OKAZAKI, Y., MURAMATSU, M., INOUE, Y., KIRA, A., AND HAYASHIZAKI, Y.
 RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL 20530913
 MEDLINE 11076861
 PUBMED 11076861

TITLE
 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE
 4

AUTHORS
 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL
 6 (bases 1 to 2978)

REFERENCE
 5

AUTHORS
 Akachi, S., Furuno, M., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Hayatsu, N., Hiramoto, K., Hirooka, I., Kasukawa, T., Hayashida, K., Hayashi, N., Itoh, M., Kagawa, I., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Kondo, S., Kono, H., Konda, M., Kato, H., Kawai, J., Kojima, Y., Koyama, T., Miyazaki, A., Murata, M., Koyama, S., Kurihara, C., Matsuyama, T., Numata, K., Ono, M., Ohnishi, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohtsuka, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
 Direct Submission

JOURNAL
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 Location/Qualifiers

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 /tissue_type="spinal ganglion"
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 /dev_stage="12 days embryo"
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 putative"

misc_feature
 ORIGIN

Query Match 18.1%; Score 398.6; DB 11; Length 2978;
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 Matches 892; Conservative 0; Mismatches 659; Indels 8; Gaps 3;

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 508 TCCTAGCAACAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
 368 TCTGAGCTTCAACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
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 963 GAGGAG 1022
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 1083 TCTATCGAG 1142
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Db      1320  AGAGAGAGAGAGAGATTAACCGGAGAGAGTGGAGCGCGCTGCTCAAGAGAGTGGCAGAG 1379
QY      1528  AATTCAGATGATTAATCTTCAAGAGAGAGAGAAATATTTGACAGGCTCTTCTTGGCTA 1587
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QY      1648  TCTTTAAACATCAACTTCTGCTGCTGAGAGTGGCTTAAATGAACCCCATTTGTGTC 1707
Db      1500  TTTTCAGAGAACTGAATTTCAAGCGCGCTGGAGTGGCATGCTAGACCACTTTTAAAGC 1589
QY      1708  CAGACCTTCAGTGTGTTATGCAAGAGACATGCTGTAATGATGATTTCTGAGGTTTC 1767
Db      1560  CTGATCCCGAGGCTATTATTCAGAGAGATGCTGAGACATGAACAGTCTCTACAGTTA 1619
QY      1768  GGGGGGTGGAATTTGATGACAGAGATAGAGAGTCTTCAAAACTTTGACAGAGTCTG 1827
Db      1620  AAGGTGTGATCTGAGAGCCCAAGACCAAGCTTTTCAAGAGAGTGGCCAGAGCAGTGT 1679
QY      1828  TTCTTAATGATGATGAGAGAGAGATTAAGAGAGAGAGTGTGAGAGAGATGATGAC 1886
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RESULT 2
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DEFINITION   Mus musculus G protein-coupled receptor kinase 6, mRNA (cDNA clone
IMAGE:5328461), containing frame-shift errors.
ACCESSION    BC057206
VERSION      BC057206.1  GI:34784381
KEYWORDS     HTC.
SOURCE       Mus musculus (house mouse)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
AUTHORS      Strausberg, R.L., Feingold, E.A., Grouse, L.H., Dege, J.G.,
1 (bases 1 to 2989)

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TITLE
JOURNAL      JOURNAL
MEDLINE      22388257
PUBMED       12477932
REFERENCE    2 (bases 1 to 2989)
AUTHORS      Strausberg, R.
TITLE       Direct Submission
JOURNAL     Submitted (29-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

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REMARK
COMMENT      Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

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FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:5328461"
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Clone distribution: MGC clone distribution information can be found
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Series: IRAX Plate: 123 Row: m Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7242151
This clone has the following problem: frame shifted.
Location/Qualifiers

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ORIGIN

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Query Match      17.1%; Score 376; DB 11; Length 2989;
Best Local Similarity 54.8%; Pred. No. 3.3e-72;
Matches 883; Conservative 0; Mismatches 700; Indels 27; Gaps 6;

QY      280  CTTGCTCAAGCCATGCTGAGCATGAGGAGCCCTGAGCAACTGATGCAACGCGCTTACC 339
Db      145  CGGACCGGGCGGCGCTGAGCCCATGAGAGCTCGAGAAATGCTAGCAACAACGATGCTAC 204
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Db      205  TCAAGTCCCGGAGAGGTGTGCTGCGGATGCAAGAGCAAGAGCAAGATGAGCGCGAGA 264
QY      397  GCCTGAGCCCTGCGGAGCTGAGAGGCTGCGGAGAGTCCGCCAAGACTGCTCCGAACT 456
Db      265  TGTCTCAATTTCCCATATCAAGCAAGTGAAGAGTGTGACTGACTGAGCGCTGAGACT 324
QY      457  TCCACAGCTGTGTGAGAGAGCCCATGAGTGGCGGCTCTTCCGTAATCTTACAGCA 516
Db      325  ACCACAGCTATGTGAGCGCAGCCCATTTGGGCGCTGTATTTTCGTAATCTTGTGCTA 384
QY      517  CAGTCCCAAGCTTCCGCAAGGCGGCAACTTCTTGAAGAGAGTGCAGACACTGGAAGCTG 576
Db      385  CGAGACTGAGCTGACCCCGGTGTACTCTTCTGGAATGCGGAGTGTGTAATGAGTGA 444
QY      577  CCGAGAGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 636
Db      445  CCCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501
QY      637  CCCCTGCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696

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Db	502	ACACGGGCTCTGACTCATCTCCCTGAAGTTTCCACGSCAGCTGTAAGTAAAC-TGAGCCCAAG	560
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Qy	757	CTTCTCTTGCAGAGCAGCCCTTTTAAGATTTTGAGACGAGGGCTCTTACAGCAAGTTTC	816
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Qy	817	TGCAGTGGAAACCTTTCGAGATGACCAAGTGTCAAGACAGTACTTCACTGAGTTCCAGAG	876
Db	679	TGCAGTGGAAAGTGGCTGGAAGAGCAACAGTGAACAAAAACACTTTCAGAGGATCCAGAG	738
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Qy	937	TGTATGCTGTAAAGAACTTGGACAAAGAGCGCTGAGAGAAAGGTGGCGAGAAATGG	996
Db	784	TGTATGCAATGCAAGAACTGGAAAAAGGAGATTAAGAACACAAAGGGAGGCGCATGG	843
Qy	997	CTCTTGTGAAAAGAAATCTTGGAGAGAGTCAAGAGCCCTTTCATTGTTCTCTTGAGCT	1056
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Db	904	AGGCTTATGAACCAAGATGCACTGTGCTGTGCTGTACATGATGAATGAGAGGTATGC	963
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Db	964	TAAAGTTCAACATCTCAACATGGGCGAGGCTGGCTTCTCTGAAAGCATGTGCTGTTCT	1023
Qy	1177	ACTGGGCCAGATAGCCGTGTGGAGTGTCTGCACTCCATGAATCTGGCATGTCTATGCGG	1236
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Db	1084	ATCTAAGCCAGAAATATCTCTTCTGATGACATGTGGCCACATTCGGATCTGGACCTGG	1143
Qy	1297	GGCTGGCCGTGAGATGAAAGGTGGCAAGCCCATCAACAGGGGCTGAAACCAATGGTT	1356
Db	1144	GACTGGCCGTGCATGTCCCTGAGGGGCCAGACATCAAGGCCGTGTGGGCACTGTGGCT	1203
Qy	1357	ACATGGCCCTGAGATCTCTATGSAAGAAAGTAAATTTCTTATCTGTGGACTGGTTTG	1416
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Db	1321	AGAAAGTAAAGCGGAAGGTGAGCCGGCTGTCAAGAAATGGCCGAGAAATACAG	1380
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Db	1561	AGGCTATTTATTCAGAGATGTCTGTGACATTGAAACAGTTCTTCAAGATTAAGAGTGTGG	1620

Oy		1777	AATTGATACAAAGATBAGCACTTTTCATAAACTTGGACAAGGTGCTCCATGAS	1836
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Oy		1837	CATGGCAGGAAGAATTAATGAAAACGGCACTGTTTGAGAACGTAAATGC	1886
Dd		1691	CTTGCGAATATGATGTGTGAGACCAGATGCTTCCAGAACTCATGTC	1720
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LOCUS		BX404586	Homo sapiens NEUROBLASTOMA	Homo sapiens cDNA clone
DEFINITION		CSODA004YM05 3-PRIME, mRNA sequence.		
ACCESSION		BX404586		
VERSION		EST.		
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SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		1 (bases 1 to 1201)		
JOURNAL		Li W.B., Gruber C., Jessee J. and Polayes D.		
COMMENT		Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3090.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSOAA004AG03NP1&cluster=3090.f . Contact : Feng Liang Email : fliang@life tech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOAA004AG03NP1. Location/Qualifiers 1..1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODA004YM05" /tissue="NEUROBLASTOMA" /issue_lib="Homo sapiens NEUROBLASTOMA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
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source				
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Dd		884	TAAAGATGATGCTCGCAAGAGCTAGAGAAAACCGGATCCAAGAGCGGAAAGGAGAGGC	825
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QY	1052	GGCCGACGCTTTGAGAGCAAGACCCATCTTGCCTTGCATGAGCCTGATGATGGGCG	1111
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Db	704	CGACCTCAATTTCCACATCTTCAACAGGTGGGAGCCGAGCTGGCTTCCCGAAGCCGGGCGCT	645
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QY	1592	ACCAAGAGCAACGCTTAGAGAGCAAGAAAAGTCTGATGATCCAGAAACATATTTCTT	1651
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QY	1652	TAAAGCATCAACTTCTCTGCTGGAGAGCTGCGCTTAATTGAACCCCATTTGTGCAGA	1711
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Db	107	C 107	
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DEFINITION	Homo sapiens, similar to G protein-coupled receptor kinase 2-like		
ACCESSION	BC027597		
VERSION	BC027597.1	GI:20379554	
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2329)		
JOURNAL	Strasberg,R.		
REMARK	Direct Submission		
COMMENT	Submitted (08-APR-2002) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgsbds-remail.nih.gov		
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
	cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki		

Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbio.org
 Ampu Madan, Jessica Pahay, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 34 Row: i Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4885346
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 Location/Qualifiers

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Best Local Similarity	57.4%; Pred. No. 5,9e-58;		
Matches 623; Conservative	0; Mismatches 454; Indels 9; Gaps 3		
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QY	827 ACTCTCGAGAGGACACAGAGTGCAGACAAAGTACTTCACTGATTCAGAGTGTGGGGAA	886	
DB	981 ATGGCTGGAAGGCAACCGGTACAAAGAACACATTTAGACATTAACAGGTTCTTAGGAAA	1040	
QY	887 AGGTGTTTTGGGGAGGTATGTGCGCTCAGGTGAAACAACTGGGAAAGATGATGCTG	946	
DB	1041 AGCGGATTTGGAGAGGTTTGGCGCTGTCAAGTGTGACACACAGAAAGATGATGCTG	1100	
QY	947 TTAGAAACTCGACCAAGCGCTGAAGAAAGAGGTGGGAGAGATGCTCTTGTGA	1006	
DB	1101 CAAAAAGCTACAAAAAAGATTAAGAAAGAGAAAGATGATGAGTATGCTTAAATGA	1160	
QY	1007 AAAAGAAATCTTGAGAGAGGTGAGAGCCCTTTCATGTGTCTCTGTGGCTATGCTTTGA	1066	
DB	1161 GAAAGAAATTTCTGAGAAAGTGCMAAGTAGATTTCTAGTTAGTTTAGCTTACGCTTATGA	1220	
QY	1067 GAGCAAGACCCATCTGCGCTGTTCATGACCTTGATGAATGGGGAGACCTCAAGTTCA	1126	
DB	1221 AACCAAGATCCTTGTGCTGTGTGTCTCAACATTAATGAATGAGGGGATTTGAAGTTTCA	1280	
QY	1127 CATCTACAAAGCGTGGGACCGCGTGTCTGACATGAGCCGGGTATCTTTACTGCGCCCA	1186	
DB	1281 CATTTACAACCTGGGCAATTCGCCGCTTTATGAGAGAGAGCCGATTTTCTATGTGTCAGA	1340	
QY	1187 GATAGCTGTGGGATCTGCACTCCATGATCACTGGGCAATGTCATTCGGGACATGAAAGCC	1246	
DB	1341 GCTGTGTGGCGCTTGGAGAGATTTACAGAGGAAAGATTTGATACAGACCTTGAGACC	1400	
QY	1247 TGAAGATGTGCTTCTGATGACCTGGCAACTGCAAGTTATTTGAACCTGAGGCTGGCCGT	1306	
DB	1401 TGAAGATTTCTCTTGAATGATGATGACATCCGAGATTTTCAGACTCGGTTTGGCCAC	1460	
QY	1307 GGAATGGAAGGATGGCAACCCATCAACCAAGGGCTGGAACCAATGGTTATCAATGCTCC	1366	
DB	1461 AAGATCCCAAGAGACACAGAGGTTGAGAGAGAGTTGGAACAGTGGCTTACATGGCAC	1520	
QY	1367 TGAATCTTAAGAAAAAGTAAATTAATTCATCTGTGAGCTGTTTGCATCGGATG	1426	
DB	1521 TGAAGTTGTCA--ATAATGAAAGATGATCGTTATAGTCCCATTTGTGTGGAAATTGCTTG	1577	

QY 1427 CAGCATTTATGAAATGCTGTGAGCAACACCATTTAAAGATTACAGAGAAAGCTGAC 1486
 DB 1578 TCTGATCTGTAATGATTCAGGACATTTCTCATTTAAATAATACAGAGAAAGCTCA 1637
 QY 1487 TAAAGAGATCTGAAAGCAAGATCTGCAACAGAGATCAATTCACAGATTAATCTT 1546
 DB 1638 ATGGAGAGAGTCTGATCAAGAA---TCAAGATATATACAGAGATATTTGAGAACTT 1694
 QY 1547 CACAGAGAGCAAAAGATTTGACAGCTCTTCTTGTGCTAAGAAACAGAGCAAGCTT 1606
 DB 1695 TTCAAGAGATGCTCAATCTATCTGAGATGTTACTACAGAGATTCAGAGAGCGGCT 1754
 QY 1607 AGAAGAGCAAGAAAG---TCTGATGATCCAGAGAAATCATTTCTTTAAAGATCA 1663
 DB 1755 GGGCTGCGAGGCGAGAGAGCGGCTGGGAGTGAAGAGCAAGCGCTGTTCAAGAGATCA 1814
 QY 1664 CTTTCTGCTGCTGGAAGCTGCGCTTAATTGAACCCCATTTGTCAGAGACCTTGAGTGT 1723
 DB 1815 CTTGAGAGAGCTGAGAGCAACATGCTGAGAGCCCTTTCTGCTGATCTTCAATGCGCT 1874
 QY 1724 TTATGCCAAAGACATGCTGAAATTTGATGATTTCTGAGGTTGCGAGGCTGAAATTTGA 1783
 DB 1875 TTACTGTAAGAGCTGCTGAGATTCAGAGAGTTCTGCGGCTGAAAGGATCTACCTGA 1934
 QY 1784 TGACAAAGATAGCACTTCTTCAAAAATTGCGACAGAGTCTGTTCTATAGCATGCA 1843
 DB 1935 CACGCGATGAGAGCTTCTATGCTGCTGTTGCTACCGGCTGTGTCTTCATCCCTGCA 1994
 QY 1844 GGAAGA 1849
 DB 1995 GAATGA 2000

RESULT 5

EX392018/c 917 bp mRNA linear EST 13-MAY-2003
 LOCUS EX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CSODL010YD11 3-PRIME, mRNA sequence.

ACCESSION EX392018 GI:30607809
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 917)
 LA,W,B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSDBAI046ZH12_CS04416_1&cluster=3090.f.
 Contact: Peng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CSDBAI046ZH12_CS04416_1.

FEATURES

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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="CSODL010YD11"
 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /cell_line="RAMOS CELL LINE"
 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)

ORIGIN

primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 14.0%; Score 307; DB 13; Length 917;

Best Local Similarity 63.8%; Pred. No. 5e-57;

Matches 482; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

QY 749 GGCATGCTCTTCTGCAAGACAGCCCTTTAAGATTTGCGACCGAGCCCTTACGA 808
 DB 796 GACCAACAGATGACTGAGCGTGGCCCTTTTCCGACTCTGACAGCATCTTAA 737
 QY 809 CAAGTTCTGAGTGAAGAACTCTGAGATGCAACAGTGTGACAAATCTTCACTGA 868
 DB 736 CCGTTCTCTGAGTGAAGTGGCTGGAAGGCGCAGTGAACAAAACCTTCAGGCA 677
 QY 869 GTTCAAGTGTGAGGAGAGTGTGTTTGGGAGAGTGTGCTCCAGGTGAAAACAC 928
 DB 676 ATACGAGTCTGGGCAAGGTGGCTTTGGGAGAGTGTGCGCTCCAGGTGCGGCGAC 617
 QY 929 TGGGAAGATGATGCTGTGTAAGAACTGGAACAGAGCGGCTGAAGAGAGGTGCGCA 988
 DB 616 AGGTAAAGATGATGCTGTGCAAGAGCTGAGAAAGAGAGAGAGAGAGAGAGAG 557
 QY 989 GAAGATGCTCTTGGAAAGAAATCTTGAAGAGTGAAGAGCCCTTCAATTGCTTC 1048
 DB 556 GGCATGAGGCTGCAACAGAGAGAGATCTTGAAGAGTGAAGAGTGTGATGAG 497
 QY 1049 TCTGCTATGCTTTGAGAGCAAGACCATCTGCTGTTGATGACACCTGATGATAG 1108
 DB 496 CTTGCTCTAGCTATGAGACCAAGAGAGCGCTGTGCTGTGCTGACATGATGAGAG 437
 QY 1109 GGGAGACCTCAAGTTCCACATCTCAACAGTGGGACCGCTGCTGCAATGAGCGGCT 1168
 DB 436 GGGGACCTCAAGTTCCACATCTCAACATGAGGACGAGCTGCTGCCGAGAGCGGCG 377
 QY 1169 GATCTTTTACCTGAGCCAGATAGCCTGTGAGATGCTGACCTTCATGAATCTGGCATCT 1228
 DB 376 GCTCTTCTAGAGCGCGCGAGATCTGCTGCTGAGAGATCTGACCGGAGCGCATCTG 317
 QY 1229 CTATGCGACATGAAGCTGTGAGATGTGCTTGTGATGATCTGCGCATCTGACATGATC 1288
 DB 316 GTACAGGACCTGAAGCCCGAGAAATCTTGTGTGATGACACAGGCGCATCTGCACTCT 257
 QY 1289 TGACCTGGGCGCGCGTGAAGTGAAGGAGTGAAGCCCATCAACAGAGGCTGAGAC 1348
 DB 256 TGACCTGGGCGCGCGTGAAGTGAAGGAGTGAAGCCCATCAACAGAGGCTGAGAC 197
 QY 1349 CAATGTTACATGCTCTGTGATCTTAATGAGAAAGTAAATTTCTATCTGTGCA 1408
 DB 136 CGTGGTTACATGCTCTGTGAG---GTGGTGAAGAAATGAACGCTACACCTTCAGCCTGA 140
 QY 1409 CTGCTTTCCATGAGATGAGATCTTATTAATGATGCTTGTGAGCAACCATTAAGA 1468
 DB 139 CTGGTGGGCGCTGCTGCTCTCTGATGAGATGATGCAAGGCGAGTCCCTTCACGA 80
 QY 1469 TTAACAGAAAGGTCAGTAAAGAGATCTGAAGC 1503
 DB 79 GAGAGAGAGAGATCAAGCGGAGAGAGATGAGC 45

RESULT 6

AY406080 1721 bp DNA linear GSS 15-DEC-2003

LOCUS AY406080 Homo sapiens GPRK5 gene, VIRUTAL TRANSCRIPT, partial sequence,

DEFINITION AY406080 genomic survey sequence.

ACCESSION AY406080 GI:39762054

VERSION GSS.

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1721)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1721)
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment
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1..1721
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1721
/gene="GPRK5"
/locus_tag="HCM2438"

Query Match 13.9%; Score 304.6; DB 29; Length 1721;
Best Local Similarity 49.5%; Pred. No. 2e-56;
Matches 559; Conservative 0; Mismatches 561; Indels 9; Gaps 3;

QY 759 TTCTTGAAGAAGAGCCCTTTAAGATTTCGTGACAGCGCTTCAACAGAAATTTCG 818
DB 402 TACCTGAGGGGAGAACATTCACGATATCTGAGACACATGTTTTCACCGCTTTC 461
QY 819 CAGTGGAACTCTTCAGATGCAACAGTCTCAACAAGTACTTCACTGAGTTCAGAGT 878
DB 462 CAGTGGAACTCTTCAGATGCAACAGTCTCAACAAGTACTTCACTGAGTTCAGAGT 878
QY 879 CTGGGGAAGGTGTTTGGGAGGTATGTGCGCTCCAGGTGAAAACTCTGGAAATG 938
DB 522 NNN 521
QY 939 TATGCTGTAAAGAACTGACACAGACCGCTGAGAGAAAGAGTGGCCAGAAAGTGGT 998
DB 582 TATGCTGTAAAGAACTGACACAGACCGCTGAGAGAAAGAGTGGCCAGAAAGTGGT 998
QY 999 CTCTTGAAGAAAGAAATCTTGAAGAGTTCAGACCGCTTTCATTTCTCTGCGCTAT 1058
DB 642 CTCAATGAGAACATCTTCGAGAGTCAACAGTCAAGTTGTGCTCAACCTGGCTAT 701
QY 1059 GCTTTGAGAGCAAGACCATCTCTGCTTTCATGAGCTGATGATGGGGAGACTTC 1118
DB 702 GCTTGAAGACCAAGATGACATGTGCTTGTGCTGACATCAATGATGGGGAGACTTC 761
QY 1119 AAGTTCACATCTAACAGCTGGGACGCTGAGCAATGAGCGGGGTATCTTTTTC 1178
DB 762 AAGTTCACATCTAACAGCTGGGACGCTGAGCAATGAGCGGGGTATCTTTTTC 821
QY 1179 TCGGCCCAATAGCTGTGGAGTGTGACCTTCATGAACTCGGCATGTCTATCGGAC 1238
DB 822 GCGGAGAGATCCTTGCGGCTTAGAGACCTCCACCGTAGAAACACGCTTACCGAGAT 881
QY 1239 ATGAGCTGAGATAGTGTCTTGTGATGACCTCGGAACTGAGGTATCTGACCTGGG 1298
DB 882 CTGAACCTGAAAAATCTCTTGAATGATTTATGAGCCATTTAGATCTCGACCTGGGC 941
QY 1299 CTGGCCGTGAGATGAAGGCTGGCAAGCCCATCAACCGAGGCTGAGAACCAATGTTTC 1358
DB 942 TTGGCTGTGAGATCCCGAGGAGACCTGATCCGCGCGGGGTGGGACCTGTTGGCTAC 1001

QY 1359 ATGCTCTGAGATGCTTAATGAAAAAGTAAGTTATTTCTATCTGTGATCGTTTGGC 1418
DB 1002 ATGCTCTGAGATGCTTAATGAAAAAGTAAGTTATTTCTATCTGTGATCGTTTGGC 1058
QY 1419 ATGAGTGAAGCATTTATGAAATGTTGCTGAGCAACCATTTCAAAAGATTACAGAA 1478
DB 1059 CTGCTGCTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
QY 1479 AAGTTCACATCTAACAGCTGGGACGCTGAGCAATGAGCGGGGTATCTTTTTC 1538
DB 1119 AAGTTCACATCTAACAGCTGGGACGCTGAGCAATGAGCGGGGTATCTTTTTC 1178
QY 1539 GATTAATCTCAAGAGAAAGCAAAAGATTTATTCAGAGCTCTTCTTGTCTAAGAACTGAG 1598
DB 1179 ---AAGTTCCTCGAGAGAGCCAGATTCATCTGCAAGATGCTGCTCAAGAAAGTCCGAG 1235
QY 1599 CAAGCTTGAAGAGCAAGAAAG---GTCTGATGATCCAGAAACATCTTTTAA 1655
DB 1236 CAGAGGCTGGCTGCTGAGAGAGAGGAGGCTGAGAGTCAAGAGACCCCTTCTTCAAG 1295
QY 1656 ACATCACTTCTCTCGCTGAGAGTGGCTTAATGAAACCCCAATTTGTCAGACCT 1715
DB 1296 AAGTGAACCTTCAAGCCTTGAAGAGCGGATGTTGACCTTCTTCCAGACNNN 1355
QY 1716 TCAGTGTGTTATGCAAGACATCCGCTGAATGATGATTTCTCTGAGGTTGGGGGTG 1775
DB 1356 NNN 1415
QY 1776 GAATTTGATGACAAAGTAAAGAGTCTTCAAAAACCTTGGCAGAGTGTGTTCTATA 1835
DB 1416 NNN 1475
QY 1836 GCATGCAAGAAATATTATGAAACGAGACTGTTGAGAACTGATG 1884
DB 1476 NNN 1524

RESULT 7
LOCUS B0057469 1058 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
ACCESSION B0057469
VERSION B0057469.1 GI:19816809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1058)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lou Straud
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>
Plate: LICK2064 row: j column: 03
High quality sequence stop: 631.
FEATURES
source Location/Qualifiers
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/clone="IMAGE:5813090"
/tissue_type="Lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"

/clone_11b="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 13.7%; Score 300.2; DB 13; Length 1058;
 Best Local Similarity 63.9%; Pred. No. 1.7e-55;
 Matches 471; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

749 GGCCATGAGCTTTCTTGCAGAGCAGCCCTTAAAGATTCTGTGACAGAGCCCTTCTACGA 808
 5 GACCCAGAGTACTAGAGGTGGCCCTTTTGGCCAGTACTGACAGCATCTACTTCAA 64
 809 CAAGTTCTGACAGTGAATCTTTCAGATGACCAAGTGTGACAGTACTTCTACGA 868
 65 CCGTTTCTGACAGTGAATGAGTGGTGAAGAGCCAGTGTGACCAAGTGTGACAGCA 124
 869 GTTACAGAGTCTGGGAGAAAGTGTGTTGGGAGGATGTCGCGTCCAGGTGAAGAAC 928
 125 ATACCGAGTCTGGGAGAAAGTGTGTTGGGAGGATGTCGCGTCCAGGTGGCCAC 184
 929 TGGGAAGATGATGCTGTGAAGAACTGACAGAGAGCGCTGAGAGAAAGAGTGGCGA 988
 185 AGTGAAGTATGCTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
 989 GAAAGTGTCTCTCTGAGAAAGAAATCTTGAAGAGTGTGAGAGAGAGAGAGAGAGAG 1048
 245 GGCCATGAGCGCTGAG 304
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 1109 GGGAGAGCTCAAGTTCACATCTACAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 1168
 365 GGGAGAGCTCAAGTTCACATCTACAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 424
 1169 GATCTTTTACTGAG 1228
 425 CGTCTTCTAGCGCCGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 484
 1229 CTATGGGAGATGAAGCTGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1288
 485 GTACAGAGAGCTGAG 544
 545 TGACCTGGAGATGATGT 604
 1289 TGACCTGGAGATGATGT 1348
 545 TGACCTGGAGATGATGT 604
 1349 CAATGTGATCATGCTCTTGAAGATCTTGAAGATCTTGAAGATCTTGAAGATCTTGA 1408
 605 CGTGGTTATCATGCTCTTGAAGATCTTGAAGATCTTGAAGATCTTGAAGATCTTGA 1468
 1409 CTGCTTGTGATGAG 1468
 662 CTGCTTGTGATGAG 721
 1469 TTACAG 1485
 722 GAG 738

RESULT 8
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 LOCUS
 DEFINITION AGNCOURT_6662941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180

5', mRNA sequence.
 B0061148
 B0061148.1 GI:19884933
 EST.
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1019)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LINC2083 row: h column: 05
 High quality sequence stop: 704.
 Location/Qualifiers

FEATURES

source

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 /clone="IMAGE:5920180"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 13.6%; Score 299.2; DB 13; Length 1019;
 Best Local Similarity 63.8%; Pred. No. 2.7e-55;
 Matches 470; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

749 GGCCATGAGCTTTCTTGCAGAGCAGCCCTTAAAGATTCTGTGACAGAGCCCTTCTACGA 808
 5 GACCCAGAGTACTAGAGGTGGCCCTTTTGGCCAGTACTGACAGCATCTACTTCAA 64
 809 CAAGTTCTGACAGTGAATCTTTCAGATGACCAAGTGTGACAGTACTTCTACGA 868
 65 CCGTTTCTGACAGTGAATGAGTGGTGAAGAGCCAGTGTGACCAAGTGTGACAGCA 124
 869 GTTACAGAGTCTGGGAGAAAGTGTGTTGGGAGGATGTCGCGTCCAGGTGAAGAAC 928
 125 ATACCGAGTCTGGGAGAAAGTGTGTTGGGAGGATGTCGCGTCCAGGTGGCCAC 184
 929 TGGGAAGATGATGCTGTGAAGAACTGACAGAGAGCGCTGAGAGAAAGAGTGGCGA 988
 185 AGTGAAGTATGCTGTGAG 244
 989 GAAAGTGTCTCTCTGAGAAAGAAATCTTGAAGAGTGTGAGAGAGAGAGAGAGAGAG 1048
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 1049 TCTGGCTTATGCTTTGAG 1108
 305 CTGGGCTTATGCTTTGAG 364
 1109 GGGAGAGCTCAAGTTCACATCTACAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 1168

Db 365 GGGGACCTCAAGTTCCATCTACACATGAGGCGAGGCTGCTTCCCGAAGGCGGCG 424
QY 1169 GATCTTTTACTCGGCCCCAGATACCTGTCGAGATGCTGACCTTCATGAATCTCGCATCT 1228
Db 425 CGCTTCTTACGCCCCCGAGATCTGCTGTCCTGAGAGCATCTGCAACCGGAGCGCATCGT 484
QY 1229 CTATCGGACATGAGGCTGAGATGCTTCTGATGATGATCTGCGCACTGCGAGTTATC 1288
Db 485 GTACAGGACCTGAAAGCCGAGAACATCTTCTGATGATGATGATGATGATGATGATGAT 544
QY 1289 TGACCTGCGGCTGCGCTGAGATGAGGCTGAGCAAGCCCATCAACGAGGCTGAGAC 1348
Db 545 TGACCTGAGACTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
QY 1349 CAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1408
Db 605 CGTGGGTTACATGCTGCTCGGAG---GTGGTAAATAATGAAAGCTTACAGTCCCTGA 661
QY 1409 CTGGTTTCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1468
Db 662 CTGGTGGCGCTCGGCTGCTCTCTGATGAGATGATGATGATGATGATGATGATGATGAT 721
QY 1469 TTACAGAGAAAGGTC 1485
Db 722 GAGGAAGAAAGAAATCA 738

RESULT 9

AY406082

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

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Db 462 GATGAGAAATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
QY 879 CTGGGAGAAAGTGTGTTGGAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 938
Db 522 NNN 581
QY 939 TATGCTGTAAGAACTGGAACAAGCGGCTGGAAGAAAGTGGGAGAAAGTGGCT 998
Db 582 TATGCTGTAAGAACTGGAACAAGCGGCTGGAAGAAAGTGGGAGAAAGTGGCT 998
QY 999 CTCTTGAAGAAAGTGTGTTGGAGAGTATGATGATGATGATGATGATGATGATGATGAT 1058
Db 642 CTCAACGAAAGCAGATCTTGAAGAGTCAAGCCAGTGTGTGATCACTGAGCTTAT 701
QY 1059 GCTTTGAGGAGAACCCATCTCTGCTTGTCAATGAGCTGATGATGATGATGATGATGATGAT 1118
Db 702 GCTATGAAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 761
QY 1119 AAGTTCACATCTCAACAGTGGCAAGCGGCTGGAAGAAAGTGGGAGAAAGTGGCT 1178
Db 762 AAGTTCACATCTCAACAGTGGCAAGCGGCTGGAAGAAAGTGGGAGAAAGTGGCT 1178
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QY 1539 ATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
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QY 1836 ATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1884

ORGANISM	REFERENCE	AUTHORS
<i>Homo sapiens</i>		
Bakaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
1 (baes 1 to 560)		
Kim, N.-S., Hahn, Y., Oh, J.-H., Lee, J.-Y., Ahn, H.-Y., Chu, M.-Y.		

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COUNTRY	

FEATURES
source

ORIGIN

Matches 37

Db 810 AAAGTGA 816

SOURCE

D5

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/organism="Homo sapiens"
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/lab_host="HDH108" (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DX0"
/notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR 1; Site_2: Not 1;
UI-E-DX0 is a cDNA library containing the following
tissue(s): fetal eyes. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not 1 site. Double
stranded cDNA was ligated to an EcoR 1 adaptor, digested
with Not 1, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not 1 site and the (dT)18 tail. This
sequence tag for this library is AGAATCAGA. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

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High quality sequence stop: 697.

FEATURES

source

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 /clone="IMAGE:5920182"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.4%; Score 272.2; DB 13; Length 1017;
 Best Local Similarity 58.8%; Pred. No. 2.6e-49;
 Matches 526; Conservative 0; Mismatches 359; Indels 9; Gaps 3;

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 DB 1 TGGCCCTCAATGAGAGAGATCTTCGAGAGGTGCAAGTCAAGTTGTGTAACTGG 60
 QY 1054 CCTATGCTTTGAGAGAGAACCCATCTTCTGCTTCATGAGCCTGATGAATGGGGAG 1113
 DB 61 CCTATGCTTCAGAGACCAAGATGACATGCTTGTGCTTCATCATGATGAATGGGGAG 120
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 DB 121 ACTCGAAGTTCACATCTCAACAGTGGGACAGGCTGCTGCAATAGCCGGGTATCT 180
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 QY 1234 GGGACATGAAGCTTGAAATGTGCTTCTGATGACCTGAGCACTGAGATTTATGACC 1293
 DB 241 GAGATCTGAAGCTTGAAACATCTGTTAGATGAATTATGCGCACTTATGAGATCTCAAGCC 300
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 DB 301 TGGGCTTGGCTGTAAGATCCCCGAGGAGACCTGATCCGGGCGCGGCTGACTGTG 360
 QY 1354 GTTACATGCTCTGATGATCTTATGAGAAAGTAAATTATCTTATCTGTGAGCTGTG 1413
 DB 361 GCTACATGCTCTGAGGTCC--TGAACAACAAGGTACGGCTTGAAGCCCGCACTACT 417
 QY 1414 TTGCATGAGATGACGATTTATGAATGTTGCTGAGCAAGACCATTTCAAGATTACA 1473
 DB 418 GGGGCTTGGCTCTCATATGATGATGAGGCGCAGTGGCGCTTCGGCGCGCGCA 477
 QY 1474 AGAAAAAGCTGAAGAGATGTAACAACAAGAACTCTGCAAGAGGTCAATATTC 1533
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 QY 1651 TTAAGCATCAATCTTCTGCGCTGGAAGTGGCTTAATGAACCCCATTTGTGCGAG 1710
 DB 655 TCGAGACATGAATCTCAAGCGCTTTAGAGCGGAGATGTGGAACCTCTCTCTGTTCCAG 714
 QY 1711 ACCCTCAAGTGTATTAGCCAAAGACATGCTGAATGATTTCTCTGAGGTTGCGG 1770

DB 715 ACCCCCGCGCTGTACTGTAAAGAGCTGTGGACATGACAGACTTCTCAGTGTAG 774
 QY 1771 GGGTGAATTTGATGACAAAGATAGAGTCTTTAAAACTTGGAGAGGTGCTGTT 1830
 DB 775 GGGTGAATTTGATGACAAAGATAGAGTCTTTAAAACTTGGAGAGGTGCTGTT 834
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RESULT 15
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 LOCUS
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 wdt7407.x1 Soares_NRL_T-GBC_S1 Homo sapiens cDNA clone
 IMAGE:2328372 3' similar to gb:U5388 G PROTEIN-COUPLED RECEPTOR
 KINASE GRK5 (HUMAN);, mRNA sequence.
 A1934968
 A1934968.1 GI:5673838
 EST.
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 815)
 NCBI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 Seq primer: -400P from G1bco
 High quality sequence stop: 483.
 Location/Qualifiers
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 /lab_host="DH10B"
 /clone_id="NIH_MGC_99"
 /note="Organ: pooled; Vector: pT73D-Pac (pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung Nbh1.9W, testis NHT, and B-cell
 NCI CGAP GCB1) were mixed, and as circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 12.3%; Score 270.6; DB 9; Length 815;
 Best Local Similarity 62.3%; Pred. No. 5.7e-49;
 Matches 439; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

QY 759 TTTTGGCAAGAGAGCCCTTTAAGGATTTGTAACAGGCTCTTACGACAGATTCTG 818
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 QY 819 CAGTGAATCTTCTGAGATGCAACAGTGTGACAGATCTTCACTGAGTGTGAGT 878
 DB 651 CAGTGAATGTTGTAAGAGCAACCGGTGACCAAAACATTTTCAGGAGATGTGAGT 932
 QY 879 CTGGGAAAGGTGTTTGGGAGATGTGTGCGCTGCAAGTGAACCACTGGGAGATG 938
 DB 591 CTAGAAAAAGGGGCGCTGGGATGATGTGTCTGCTCCAGGTGTGGGCGCAACGGTANATG 532

538

Db	61	AAGCCCTCGACATGGGACAGGAAAGAGCTGGACGGGAGGCGGCTGAGCCTTGGCC	120
OY	411	GGGCTGGAGGGCTGGCGGAGACTCGCCAGAAAGCTGTCCCTGAACTTTCACAGCTGTGT	470
Db	121	GGGCTGGAGGGCTGGCGGAGCTTCGCCAGAAAGCTGTCCCTGAACTTTCACAGCTGTGT	180
OY	471	GAGGAGGAGGCCATGGGTGCCCTCTTTCCTGTACCTTCTTGCCACAGTGGCCACGTTT	530
Db	181	GAGGAGGAGGCCATGGGTGCCCTCTTTCCTGTACCTTCTTGCCACAGTGGCCACGTTT	240
OY	531	CGCAAGGCGGCAACCTTCTTAAAGAGACGNGAGAACTGGGAGCTGGCCGAGAGGGAAACC	590
Db	241	CGCAAGGCGGCAACCTTCTTAAAGAGACGNGAGAACTGGGAGCTGGCCGAGAGGGAAACC	300
OY	591	ACCAAGACAGCGCGCTGGCAGGGGGCTGGTGGCCACTTGTGACAGTGGCCCTGCGGGG	650
Db	301	ACCAAGACAGCGCGCTGGCAGGGGGCTGGTGGCCACTTGTGACAGTGGCCCTGCGGGG	360
OY	651	AACCCGAAACCTTCTTCACACGAGCCGTGGCCACCAAGTGCACAGAGCCACCACTGAG	710
Db	361	AACCCGAAACCTTCTTCACACGAGCCGTGGCCACCAAGTGCACAGAGCCACCACTGAG	420
OY	711	GAAAGAGGAGTGGCTGGAGTGAAGCGTGGCGAAAGGCTGGAGGCAAGGCTTTCTTGAAG	770
Db	421	GAAAGAGGAGTGGCTGGAGTGAAGCGTGGCGAAAGGCTGGAGGCAAGGCTTTCTTGAAG	480
OY	771	CAGCCCTTTAAGAGTTTCTGACAGACGCGCTTCTTACAGCAAGTTTCTGACAGTGAACCT	830
Db	481	CAGCCCTTTAAGAGTTTCTGACAGACGCGCTTCTTACAGCAAGTTTCTGACAGTGAACCT	540
OY	831	TTGAGATGACAAACAGTGTGAGCAAGTACTTCACTGAGTTCAAGTGTGCTGGGAAAAGT	890
Db	541	TTGAGATGACAAACAGTGTGAGCAAGTACTTCACTGAGTTCAAGTGTGCTGGGAAAAGT	600
OY	891	GGTTTTGGGAGAGTATGTGCGTGCAGGCTGAAGAAACACTGGGAAAGTGTATGTCTGTAA	950
Db	601	GGTTTTGGGAGAGTATGTGCGTGCAGGCTGAAGAAACACTGGGAAAGTGTATGTCTGTAA	660
OY	951	AAACTGAGCAAGAAAGCGGCTGAAGAAAGGTGGCGAAGAGTGGCTCTGTGGAAAAG	1010
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OY	1011	GAAATCTTGGAGAGAGTCAAGACGCCCTTTCATTGTCTCTGGCGCTAAGCCTTGAAGAG	1070
Db	721	GAAATCTTGGAGAGAGTCAAGACGCCCTTTCATTGTCTCTGGCGCTAAGCCTTGAAGAG	780
OY	1071	AAGAGCCATCTGTGCTCTCTCTCACTGAGCTGATGAAATGGGGGAGACTTCAAGTTCCATC	1130
Db	781	AAGAGCCATCTGTGCTCTCTCTCACTGAGCTGATGAAATGGGGGAGACTTCAAGTTCCATC	840
OY	1131	TACACGTGGGCAAGCGGTGGCTGGACATAGACCGGAGTACTTTTACTCGGCGCCAGATA	1190
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OY	1191	GCTGTGGGATGTGCACCTTCCATGAACCTGGGCATCGTCTATCGGAGCAATGAGCCTGAG	1250
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OY	1251	AATGGCTTTCGAGATGACCTGGGCAACTGAGAGTTATGTGACTTGGGGCTGGCGTGGAG	1310
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OY	1311	ATGAAGGGTGGCAAGCCCATACCAAGGGGCTGGAGCAATGGTTTAACTGAGCTCGGAG	1370
Db	1021	ATGAAGGGTGGCAAGCCCATACCAAGGGGCTGGAGCAATGGTTTAACTGAGCTCGGAG	1080
OY	1371	ATCTTAATGGAAGAGTAAAGTATTCCTATCTGTGAGCTGTGGCCATGGAGTCAAGC	1430
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Db	1141	ATTATGAAATGTTGTGGAGAACACATCTCAAAGTTACAGAAAGAGTACGTAAA	1200
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Db	1321	AGCAGAGAAAAGTGTATATCCAGAAACATCATTTCTTTAAACGATCACTTTCCT	1380
QY	1671	CGCCTGAAGAGCGCCATATGAAACCCCACTTGGGCGAACCCCTCAAGTGTATTGCC	1730
Db	1381	CGCCTGAAGAGCTGGCTAATATTAACCCCACTTGGGCGAACCCCTCAAGTGTATTGCC	1440
QY	1731	AAAGACATGCGTGAATATGATATTTCTGTAGGTTGGGGGGTGGAAATTGTAGCAAA	1790
Db	1441	AAAGACATGCGTGAATATGATATTTCTGTAGGTTGGGGGGTGGAAATTGTAGCAAA	1500
QY	1791	GATACACGTTCTTCAAAAATTGGCGACGGTGTCTTCTATAGCATGGCAGAGAA	1850
Db	1501	GATACACGTTCTTCAAAAATTGGCGACGGTGTCTTCTATAGCATGGCAGAGAA	1560
QY	1851	ATTATAGAAACGGGACGTGTTAGAACTGAATGACCCCAACAGACCTACGGGTTGTAG	1910
Db	1561	ATTATAGAAACGGGACGTGTTAGAACTGAATGACCCCAACAGACCTACGGGTTGTAG	1620
QY	1911	GAGGGTAATTCACAAAGCTGGGCGGTGTCTTGTATATGTA	1952
Db	1621	GAGGGTAATTCACAAAGCTGGGCGGTGTCTTGTATATGTA	1662

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RESULT 3
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; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
; US-09-738-894A-1

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			Gaps	0
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QY	351	AAGCCCTCGACTGCGACAGCAAAAGAGCTGCAGCGCGCGGCTGAGCTGAGCGCTTGCC	410	
Db	61	AAGCCCTCGACTGCGCAAGCAAGAAAGAGCTGCAGCGCGCGGCTGAGCTGAGCGCTTGCC	120	
QY	411	GCGCTGCAGGCGCTGCAGGAGCTCCGCGCAAGAGCTGTCCTCGAACTTCCAAAGCTGTGT	470	
Db	121	GCGCTGCAGGCGCTGCAGGAGCTCCGCGCAAGAGCTGTCCTCGAACTTCCAAAGCTGTGT	180	
QY	471	GAGCGACGCCCATCGATGCGCGCGCTTCCGTGACTTCTTGACCAAGTGCACATGTC	530	

Db 181 GAGCAGACGCCCATGCGTCCGCTCTTCCTGATCTTCTAGCCAGATGCGCCACGTTTC 240
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 Db 241 CGCAGAGCGGCAACCTTCTTAGAGAGACGTGCAAACTGCGAGCTGGCCAGAGAGGACCC 300
 QY 591 ACCAAGACGCGCGCTGAGAGGCGTGTGGCCACTGTGTGAGAGTGGCCCTGCGCGGAG 650
 Db 301 ACCAAGACGCGCGCTGAGAGGCGTGTGGCCACTGTGTGAGAGTGGCCCTGCGCGGAG 360
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 Db 361 AACCCGCAACCTTCTTAGAGAGACGTGCGAGCGCTGGCCAGAGTGGCCAGAGAGGACCA 420
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 Db 481 CAGCCCTTAAAGATTTGCTGACCAAGGCGCTTGTACCAAGTTCTGCAAGTGAACCTC 540
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 QY 1011 GAAATCTTGAGAGAGGTGACAGCCCTTCAATTGTCTCTGCGCTATGCTCTTGAAGC 1070
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 ; Sequence 1, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-964-469-1

Query Match 75.4%; Score 1657.2; DB 4; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGTGTGACATGAGGAGCCCTTGAACACCTGATGCGAAACACCGCTTACTGAGGCGCG 350
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 QY 351 AAGCCCTGAGCACTGAGCAGACAAAGAGCTGACAGCGGAGCGGTGAACTTGCACAGCTGTG 410
 Db 61 AAGCCCTGAGCACTGAGCAGACAAAGAGCTGACAGCGGAGCGGTGAACTTGCACAGCTGTG 120
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 Db 121 GGGCTGAGAGGCTGCGCGAGAGCTCCGCAAGAGCTGTCCCTGAACTTTCACAGCTGTGT 180
 QY 471 GAGCAGAGCCCATGTGCTGCGCGCTTCTCGTGACTTCTTCAAGCAAGTGCACAGCTTC 530
 Db 181 GAGCAGAGCCCATGTGCTGCGCGCTTCTCGTGACTTCTTCAAGCAAGTGCACAGCTTC 240
 QY 531 CGCAGAGCGGCAACCTTCTTAGAGAGACGTGCAAGAACTGCGAGCTGGCGGAGAGGAGCC 590
 Db 241 CGCAGAGCGGCAACCTTCTTAGAGAGACGTGCAAGAACTGCGAGCTGGCGGAGAGGAGCC 300

QY 591 ACCAAGACAGGCGCTGCGAGGCGCTGCGCACTTGTGCGAGTGGCCCTGCGCGG 650
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 QY 1011 GAAATCTTGAAGAGTCAAGCGCGCTTCTCACTGCTGCGCGCTTCTGAGAGC 1070
 Db 721 GAAATCTTGAAGAGTCAAGCGCGCTTCTCACTGCTGCGCGCTTCTGAGAGC 780
 QY 1071 AAGACCACTCTGCGCTTCTGATGAGGCTGATGAGGAGGAGCACTCAAGTTCACATC 1130
 Db 781 AAGACCACTCTGCGCTTCTGATGAGGCTGATGAGGAGGAGCACTCAAGTTCACATC 840
 QY 1131 TACACGTCGCGCAAGGTCGCTGAGCAATGAGCGGCTGATCTTTTACTGCGCGCAATA 1190
 Db 841 TACACGTCGCGCAAGGTCGAGTGCCTGAGCAATGAGCGGCTGATCTTTTACTGCGCGCAATA 900
 QY 1191 GCGTGTGGGAGTGCAGCACTGATGAGCACTGAGCACTGAGCACTGAGCACTGAG 1250
 Db 901 GCGTGTGGGAGTGCAGCACTGATGAGCACTGAGCACTGAGCACTGAGCACTGAG 960
 QY 1251 AATGTCTTGTGATGACCTCGGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAG 1310
 Db 961 AATGTCTTGTGATGACCTCGGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAG 1020
 QY 1311 ATGAAAGGTGCAAGCCCATCAACCAAGGCTGAAACCAATGCTTCACTGAGCTCTAG 1370
 Db 1021 ATGAAAGGTGCAAGCCCATCAACCAAGGCTGAAACCAATGCTTCACTGAGCTCTAG 1080
 QY 1371 ATCTAATGGAAGGATGATTTCTATCTGCTGAGCACTGCTTGTGCACTGAGCACTGAG 1430
 Db 1081 ATCTAATGGAAGGATGATTTCTATCTGCTGAGCACTGCTTGTGCACTGAGCACTGAG 1140
 QY 1431 ATTTATGAAATGCTGCTGAGCAACCAATGCAAGATTCAGAGAAAGGCTGATTA 1490
 Db 1141 ATTTATGAAATGCTGCTGAGCAACCAATGCAAGATTCAGAGAAAGGCTGATTA 1200
 QY 1491 GAGGATCTGAAGCAAGAACTCTGCAAGCAAGGCTCAAAATTCAGCATGATTACTTCA 1550
 Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGCAAGGCTCAAAATTCAGCATGATTACTTCA 1260
 QY 1551 GAGGATCTGAAGCAAGAACTCTTGTGCAAGCAAGGCTCAAAATTCAGCATGATTA 1610
 Db 1261 GAGGATCTGAAGCAAGAACTCTTGTGCAAGCAAGGCTCAAAATTCAGCATGATTA 1320
 QY 1611 AGCAGAGAAAGTCTGATGATCCAGAGAACTATTTCTTTAAAGCATCACTTCT 1670
 Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAACTATTTCTTTAAAGCATCACTTCT 1380

QY 1671 GCCTGGAAGCTGCGCTAATTGAACCCCAATTTGTGCGAGACCTTCACTGATGATTA 1730
 Db 1381 GCCTGGAAGCTGCGCTAATTGAACCCCAATTTGTGCGAGACCTTCACTGATGATTA 1440
 QY 1731 AAAGCACTGCGTAATTTGATGATTTCTGAGGTTGCGGAGGCTGAGATTTGATGACAA 1790
 Db 1441 AAAGCACTGCGTAATTTGATGATTTCTGAGGTTGCGGAGGCTGAGATTTGATGACAA 1500
 QY 1791 GATAGCAATTTCTAATAAATTTGAGAGAGTGTGCTTCTATACATGCGAGAGAA 1850
 Db 1501 GATAGCAATTTCTAATAAATTTGAGAGAGTGTGCTTCTATACATGCGAGAGAA 1560
 QY 1851 ATTATGAAACGCGACTGTTGAGAACTGATGACCCCAAGACTTACGAGGTTGAG 1910
 Db 1561 ATTATGAAACGCGACTTGTGAGAACTGATGACCCCAAGACTTACGAGGTTGAG 1620
 QY 1911 GAGGTAATTCATCCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952
 Db 1621 GAGGTAATTCATCCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662

RESULT 5
 US-09-802-117-3
 ; Sequence 3, Application US/09802117
 ; Patent No. 644456
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Milgromski, Nathaniel L.
 ; TITLE OF INVENTION: No. 644456 Human G-Coupled Protein Receptor Kinases and Polymu
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-802-117-3

Query Match 47.6%; Score 1046.8; DB 4; Length 1062;
 Best Local Similarity 99.8%; Pred. No. 2.7e-248;
 Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGATGACATGAGGCGCTGGAACAACCTGATGCGCAACCGGCTTACCTGCGAGCGG 350
 Db 1 ATGATGACATGAGGCGCTGGAACAACCTGATGCGCAACCGGCTTACCTGCGAGCGG 60
 QY 351 AACGCTTGGACCTGCGACAGCAAGAAAGCTGCAAGCGGCGGCTGAGCTTGGCGCC 410
 Db 61 AACGCTTGGACCTGCGACAGCAAGAAAGCTGCAAGCGGCGGCTGAGCTTGGCGCC 120
 QY 411 GGGCTGCAAGGCTGCGAGGCTCGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
 Db 121 GGGCTGCAAGGCTGCGAGGCTCGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 471 GAGCAGACCCCATGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
 Db 181 GAGCAGACCCCATGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 531 CGAAGGCGCAACTTCTTGAAGCACTGCAAACTGGAAGCTGCGGAGGAGGCC 590
 Db 241 CGAAGGCGCAACTTCTTGAAGCACTGCAAACTGGAAGCTGCGGAGGAGGCC 300
 QY 591 ACCAAGACAGGCGCTGCAAGGCGGCTGAGCACTTGTGCAAGGCTGCGCGCGG 650
 Db 301 ACCAAGACAGGCGCTGCAAGGCGGCTGAGCACTTGTGCAAGGCTGCGCGCGG 360
 QY 651 AACCGCAACCTTCTCAGCGCGCGCGCAACCAAGTGCAGGCGCACTGAG 710

Db 361 AACCGACACCTTCTCAGCCAGCGCTGGCCACCAAGTCCAGAGCCACCTAG 420
 QY 711 GAAGAGGAGTGTCTCAGTACAGCTGCGCAAGGCTGAGGCGCTTTCTTGCAGAG 770
 Db 421 GAAGAGGAGTGTCTCAGTACAGCTGCGCAAGGCTGAGGCGCTTTCTTGCAGAG 480
 QY 771 CAGCCCTTAAAGATTGTGTGACAGAGGCTTTCTTACAGAGTTTCTGAGTGAATC 830
 Db 481 CAGCCCTTAAAGATTGTGTGACAGAGGCTTTCTTACAGAGTTTCTGAGTGAATC 540
 QY 831 TTGAGATGACACCAAGTGTGACAGAGTCTTCACTGAGTTCAAGTGTGAGGAAAGT 890
 Db 541 TTGAGATGACACCAAGTGTGACAGAGTCTTCACTGAGTTCAAGTGTGAGGAAAGT 600
 QY 891 GGTCTTGGGAGGATGTGCTGCTGAGTGAAGAAACATCGAGAGATGTATGCTGTAG 950
 Db 601 GGTCTTGGGAGGATGTGCTGAGTGAAGAAACATCGAGAGATGTATGCTGTAG 660
 QY 951 AAATCTGACAAAGAGGCTGAAAGAAAGTGTGAGAGATGTCTTCTTGAAGAAAG 1010
 Db 661 AAATCTGACAAAGAGGCTGAAAGAAAGTGTGAGAGATGTCTTCTTGAAGAAAG 720
 QY 1011 GAATCTTGAAGAGGCTGACAGGCTTCACTGCTCTGAGCTATGCTTGAAGAGC 1070
 Db 721 GAATCTTGAAGAGGCTGACAGGCTTCACTGCTCTGAGCTATGCTTGAAGAGC 780
 QY 1071 AAGACCATCTCTGCTCTTCTATGAGCTGATGATGAGGAGAGCTTCACTGCTATC 1130
 Db 781 AAGACCATCTCTGCTCTTCTATGAGCTGATGATGAGGAGAGCTTCACTGCTATC 840
 QY 1131 TACACGTGGGCAAGGCTGCTGCTGACATGAGCCGAGTATCTTTTCTGAGCCAGATA 1190
 Db 841 TACACGTGGGCAAGGCTGCTGCTGACATGAGCCGAGTATCTTTTCTGAGCCAGATA 900
 QY 1191 GCGTGGGATGCTGACCTCCATGAATCGTCTATCGGAGCATGAGAGCTGAG 1250
 Db 901 GCGTGGGATGCTGACCTCCATGAATCGTCTATCGGAGCATGAGAGCTGAG 960
 QY 1251 AATGCTCTTGTGATGACCTCGGCAATGAGGTTATCTGACCTGAGGCTGAGGAG 1310
 Db 961 AATGCTCTTGTGATGACCTCGGCAATGAGGTTATCTGACCTGAGGCTGAGGAG 1020
 QY 1311 ATGAGGGTGGCAAGCCATCAACCAAGAG 1340
 Db 1021 ATGAGGGTGGCAAGCCATCAACCAAGAG 1050

RESULT 6

US-09-738-894A-3
 ; Sequence 3, Application US/09738894A
 ; Patent No. 6331423
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CL000636
 ; CURRENT APPLICATION NUMBER: US/09/738,894A
 ; CURRENT FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-738-894A-3

Query Match 39.5%, Score 867.4, DB 4, Length 36651.

Best Local Similarity 95.1%; Pred. No. 1.8e-203; Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCTTAAGATGAAAGGACCTCACTATAGGCTGAGGCGCGCCGAGAGGCTTTC 60
 Db 1786 GACCTTAAGATGAAAGGACCTCACTATAGGCTGAGGCGCGCCGAGAGGCTTTC 1845
 QY 61 GCGTGGGAGGAGGAGCATGACCTATGCTGTGAGTCTTCTGAGGAGCTATATAGCA 120
 Db 1846 GCGTGGGAGGAGGAGCATGACCTATGCTGTGAGTCTTCTGAGGAGCTATATAGCA 1905
 QY 121 GTCAAGCTTCTTAAGAAAGAACTCTTTCACACCTTCACAGGCTCCACAGGCT 180
 Db 1906 GTCAAGCTTCTTAAGAAAGAACTCTTTCACACCTTCACAGGCTCCACAGGCT 1965
 QY 181 ACAGACTACCTGTAATTCCTTGTGAGCTGTCTACCGGAGAAAGGAAACAGCAGCA 240
 Db 1966 ACAGACTACCTGTAATTCCTTGTGAGCTGTCTACCGGAGAAAGGAAACAGCAGCA 2025
 QY 241 GCGCTCAGACCCCTTGTGTGCTTCCCTGAGAGTGGCGCCGCTCTCAGCATGTGAGCA 300
 Db 2026 GCGCTCAGACCCCTTGTGTGCTTCCCTGAGAGTGGCGCCGCTCTCAGCATGTGAGCA 2085
 QY 301 TGAGGAGCTCTGACAACTGATGACCAACCGCTTACCTGAGGCTCGGAAAGCTTCG 360
 Db 2086 TGAGGAGCTCTGACAACTGATGACCAACCGCTTACCTGAGGCTCGGAAAGCTTCG 2145
 QY 361 ACTGCGACAGCAAGAGTGCAGCGGCGGCGGAGCTGAGCTGAGCGCGGCTGAGCA 420
 Db 2146 ACTGCGACAGCAAGAGTGCAGCGGCGGCGGAGCTGAGCTGAGCGCGGCTGAGCA 2205
 QY 421 GCTGCGGAGAGTCCGCGCAGAGCTGTCCCTGAACTTTCACAGCTGTGTGAGCAGAGC 480
 Db 2206 GCTGCGGAGAGTCCGCGCAGAGCTGTCCCTGAACTTTCACAGCTGTGTGAGCAGAGC 2265
 QY 481 CCATGAGTGGCGGCTCTTCCGTGACTTCTTACGCAAGTGTCCCAAGGCTGAG 540
 Db 2266 CCATGAGTGGCGGCTCTTCCGTGACTTCTTACGCAAGTGTCCCAAGGCTGAG 2325
 QY 541 CAACCTTCCTAAGAGAGCTGTGAGAACTGAGAGCTGAGGAGGAGGAGGAGCA 600
 Db 2326 CAACCTTCCTAAGAGAGCTGTGAGAACTGAGAGCTGAGGAGGAGGAGGAGCA 2385
 QY 601 GCGGCTGACAGGAGCTGTGAGCACTTGTGAGAGTGTCCCTGCGGAGAAACCGGCAAC 660
 Db 2386 GCGGCTGACAGGAGCTGTGAGCACTTGTGAGAGTGTCCCTGCGGAGAAACCGGCAAC 2445
 QY 2446 CTTCTCAGACAGGCGCTGTGACCAAGTGCAGAGCAGCAGCAGCAGGAG 2505
 Db 2446 CTTCTCAGACAGGCGCTGTGACCAAGTGCAGAGCAGCAGCAGCAGGAG 2565
 QY 721 TGGCTGAGAGAGAGCTGTGAGCAAGGCTGAGGAGCAGTCTTCTGAGAGAGCAGCTTGA 780
 Db 2506 TGGCTGAGAGAGAGCTGTGAGCAAGGCTGAGGAGCAGTCTTCTGAGAGAGCAGCTTGA 2565
 QY 781 AGATTTCTGACAGAGCCTTCTTACAGCAAGTGTCTGAGTGAATCTTGTGAGATG 840
 Db 2566 AGATTTCTGACAGAGCCTTCTTACAGCAAGTGTCTGAGTGAATCTTGTGAGATG 2625
 QY 841 AACCAAGTGTGACAGAGTCTTCTTACAGTGTGAGAGTGTGAGGAGGAGTGTGAGG 900
 Db 2626 AACCAAGTGTGACAGAGTCTTCTTACAGTGTGAGAGTGTGAGGAGGAGTGTGAGG 2685
 QY 901 AGTATGTGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941
 Db 2686 AGTATGTGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2726

RESULT 7

US-09-964-469-3
 ; Sequence 3, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 4; Length 36651;

Best Local Similarity 95.1%; Pred. No. 1.1e-203;

Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GACCTTAAGTGAAGGAACTTCACTATAGGCTCGAGCGCGCCGCGAGGTCTTTC 60
 DB 1786 GACCTTAAGTGAAGGAACTTCACTATAGGCTCGAGCGCGCCGCGAGGTCTTTC 1845
 QY 61 GCTTTGGAGGTGGAGCATCTATCTGTGAGTCTCGCGGCTATATCATAGCA 120
 DB 1846 GCTTTGGAGGTGGAGCATCTATCTGTGAGTCTCGCGGCTATATCATAGCA 1905
 QY 121 GTCAAGCTTCTACAAAAGAACTCTTTCACACCTTCACAGGCTCCCAACAGGCC 180
 DB 1906 GTCAAGCTTCTACAAAAGAACTCTTTCACACCTTCACAGGCTCCCAACAGGCC 1965
 QY 181 ACAAGACTCACTGTAAATCCCTTGAAGTGTCTGACCCGCGAAGGAAAAGACAGCA 240
 DB 1966 ACAAGACTCACTGTAAATCCCTTGAAGTGTCTGACCCGCGAAGGAAAAGACAGCA 2025
 QY 241 GGCCTCCAGGCTCTTGTGCTTTCCCTGGAAGTGGCGCCGCTGCTAGCATGTGACA 300
 DB 2026 GGCCTCCAGGCTCTTGTGCTTTCCCTGGAAGTGGCGCCGCTGCTAGCATGTGACA 2085
 QY 301 TGGGGGCTCTGGAACAACCTGATCGCAACCGCCTTACCTGAGCGCCGGAAGCCCTCGG 360
 DB 2086 TGGGGGCTCTGGAACAACCTGATCGCAACCGCCTTACCTGAGCGCCGGAAGCCCTCGG 2145
 QY 361 ACTGCGACAGCAAAAGAGCTGCAAGCGCGCGGCGTGAAGCTTGCCTGCGCGCTGCAAG 420
 DB 2146 ACTGCGACAGCAAAAGAGCTGCAAGCGCGCGGCGGCGTGAAGCTTGCCTGCGCGCTGCAAG 2205
 QY 421 GCTGCGGAGAGCTCCGCCCAAGAGTGTCCCTGAATCTTCAACAGCTGTGTGAGCAGCAGC 480
 DB 2206 GCTGCGGAGAGCTCCGCCCAAGAGTGTCCCTGAATCTTCAACAGCTGTGTGAGCAGCAGC 2265
 QY 481 CCATGGTGGCGGCTCTTCCGTGAGCTTCTTGAAGCAAGTGGCCAGCTTCCGCAAGCGCG 540
 DB 2266 CCATGGTGGCGGCTCTTCCGTGAGCTTCTTGAAGCAAGTGGCCAGCTTCCGCAAGCGCG 2325
 QY 541 CAACCTTCTTGAAGAGCTGCAAGACTGGAAGTGTGAGAGTGTGAGAGCAAGCAAGCA 600
 DB 2326 CAACCTTCTTGAAGAGCTGCAAGACTGGAAGTGTGAGAGTGTGAGAGCAAGCAAGCA 2385
 QY 601 GCGGCTGCAAGGCGCTGTGAGCACTTGTGAGAGTGTGAGAGTGTGAGAGCAAGCAAGCA 660
 DB 2386 GCGGCTGCAAGGCGCTGTGAGCACTTGTGAGAGTGTGAGAGTGTGAGAGCAAGCAAGCA 2445
 QY 661 CTTTCTCAGCGAGCGCTGCGCAAGTGTGCAAGAGCAAGCAAGTGTGAGAGCAAGCAAG 720

DB 2446 CTTTCTCAGCGAGCGCTGCGCAAGTGTGCAAGAGCAAGCAAGTGTGAGAGCAAGCAAG 2505
 QY 721 TGGCTGAGTGAAGGCTGTGGCAAGCTGAGGCTTCTTGTGCAAGCAAGCAAGCAAGCAAG 780
 DB 2506 TGGCTGAGTGAAGGCTGTGGCAAGCTGAGGCTTCTTGTGCAAGCAAGCAAGCAAGCAAG 2565
 QY 781 AGATTTCTGACAGCGGCTTCTTGAAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 840
 DB 2566 AGATTTCTGACAGCGGCTTCTTGAAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2625
 QY 841 AACAGTGTGACAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 900
 DB 2626 AACAGTGTGACAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 2685
 QY 901 AGATTTCTGACAGCGGCTTCTTGAAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 941
 DB 2686 AGATTTCTGACAGCGGCTTCTTGAAGCAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 2726

RESULT 8

US-08-464-954A-2

; Sequence 2, Application US/08464954A

; Patent No. 6255069

; GENERAL INFORMATION:

; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,

; APPLICANT: PRIYA

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jane Massey Licata, Esq.

; STREET: Woodland Falls Corporate Park

; STREET: 210 Lake Drive East, Suite 201

; CITY: Quarry Hill

; STATE: NJ

; COUNTRY: USA

; ZIP: 08002

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,954A

; FILING DATE: Herewith

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/076,084

; FILING DATE: June 11, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Jane Massey Licata

; REGISTRATION NUMBER: 32,257

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (609) 779-2400

; TELEFAX: (609) 779-8488

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2848

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; ANTI-SENSE: NO

US-08-464-954A-2

Query Match 19.1%; Score 419.8; DB 3; Length 2848;

Best Local Similarity 56.2%; Pred. No. 1.1e-93;

Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

QY 305 GGCCTTGAACAACCTGATGCGCAACACGCTTACCTGCAAGGCCGGAAGCCTTGGAGCTG 364
 DB 65 GGAGCTGGAACATCTGTAGGAAACAGGTGCTACTCAAGGCCCGGGAAGGTGGCGTGG 124

QY 365 CGACAGCAAG--AGCTGACGGGCGGCGGTAGCCTGACCTGCGGCGCTGCAAGG 421
Db 125 AAATCGCAAGGCAAGCAAGAAATGCGCGAGATGCTCAAGTTCTCCCTCACTACCA 184
QY 422 CTGGCGGAGACTCGGCGCAAGAGCTGCTCCCTGAACTTCCACAGCTGTGTGACAGAGCC 481
Db 185 GTGGCAAGAGCTCGGCTGACGCTCGAGCTGATATACAGAGCTGTGTGAGAGCGGCAAGC 244
QY 482 CATGAGTCGCGGCTCTTCTGTAATTTCTTAAGCAAGTGTCCCAAGCTTCCGCAAGCGGC 541
Db 245 CATGGGCGGCTGCTTCTTCCGAGAGTTCTGTGCAAGAGCGGAGAGCTGAGCGCTGTGCT 304
QY 542 AACCTTCTGAGAGAGTGTGCAAGACTGGAGCTGTGCGGAGAGAGAGAGAGAGAGAG 601
Db 305 CGCTCTTCTGAGAGAGAGTGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
QY 602 CGCGCTGAGAGAGAGTGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
Db 365 TGAGCGGAGAG--TAAAGCAAGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
QY 662 CTTCCTGAG 721
Db 422 GGTGCGGAG 480
QY 722 GGTGAG 781
Db 481 ACCCTTCTGAG 538
QY 782 GAGTTTGTGAG 841
Db 539 CGACTACTGAG 598
QY 842 ACCAGTGTGAG 901
Db 599 GCGAGTGTGAG 658
QY 902 GGTATGTGCGGCTGAG 961
Db 659 GGTGTGCGGCTGAG 718
QY 962 GAAGCGGCTGAG 1021
Db 719 AAGGCGAGTCAAG 778
QY 1022 GAAGTGTGAG 1081
Db 779 GAAGTGTGAG 838
QY 1082 CTGCTGTGTGAG 1141
Db 839 GTGCTGTGTGAG 898
QY 1142 CAGCGTGTGAG 1201
Db 899 CAGGCTGTGAG 958
QY 1202 GCTGAGCTGTGAG 1261
Db 959 GAGGAGCTGTGAG 1018
QY 1262 GAGTGTGAG 1321
Db 1019 GAGTGTGAG 1078
QY 1322 CAGGCGGCTGAG 1381
Db 1079 CAGGCGGCTGAG 1135
QY 1382 AAGGTAAGTGTGAG 1441
Db 1136 GAATGAGAGTGTGAG 1195

QY 1442 GGTGCTGTGAG 1501
Db 1196 GATGTGAG 1255
QY 1502 GCAAGAACTGTGAG 1561
Db 1256 GCGGCTGTGAG 1315
QY 1562 AGATATTTGAG 1621
Db 1316 ACTTGTGTGAG 1375
QY 1622 GTCTGTGTGAG 1681
Db 1376 TGCCGCGAG 1435
QY 1682 TGCCCTATGTGAG 1741
Db 1436 TGCCATGTGAG 1495
QY 1742 TGAATGTGAG 1801
Db 1496 GAGATTTGAG 1555
QY 1802 CTTCAGAACTTGTGAG 1861
Db 1556 CTACAG 1615
QY 1862 GAGAGCTTTGAG 1886
Db 1616 CGAGTGTTCAG 1640

RESULT 9

US-08-221-817-12
Sequence 12, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2204 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31..1758
 US-08-221-817-12

Query Match 19.0%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 2.5e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

```

QY 305 GGCCTGACAACTGATGCGCAACCGCTTACCTGACGCGCCGGAAGCCCTCGACATG 364
DB 33 GGAGCTCGAGAAACATGCTAGCGAACAAGTGTCTACAGAGCCCGGAAGAGTGGCGTGG 92
QY 365 CGACACCAAG--AGTGCAGCGCGCGCGCTGACCTGGCCCGCGGCTGCGAGGG 421
DB 93 AATGCGCAAGGCAAGAAAGCAAGAAATGCGCGCAGATGCTCCAGTCCCTCACAATCAGCA 152
QY 422 CTGCGCGAGCTCCGCGCAAGAGCTGTCCCTGAACTTCCACAGCTGTGTGTAGAGAGCC 481
DB 153 GTGCCAAGAGCTGCGGCTCAGCTCGAGCTGACTATCCAGCTGTGCGAGCGGACCG 212
QY 482 CATCGGTCGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTCCGCGAAGCGGC 541
DB 213 CATGGGCGCTGCTGTCTCGAGAGTCTGTGCGCAAGGCGGAGCTGAGCGCGTGT 272
QY 542 AACCTTCTAGAGAGCTGCAAGATGAGAGCTGCGCGAGAGGAGGAGCAACCAAGACAG 601
DB 273 GCGCTTCTGATGAGGAGTGGCCGAGTATGAAGTGAACCCGAGATGACAAAGCGAGCATG 332
QY 602 CGCGCTGACAGGAGCTGTGGCCACTGTGTGGAGTGTGCTTCCCGCGGAGAACCCCAACC 661
DB 333 TGGGCGGACG--TAAAGCAAGATTTCTGAGCCCAAGGAGTCTTCACTATCCCTGCA 389
QY 662 CTTCCTCAGCCAGGCGGTGGCCACCAAGTCCCAAGAGCACAACCTGAGAGAGAGCGAT 721
DB 390 GGTCCCGCGGAGCTGTGTGAGAAC-TGCACCAAGGCTGTGAGAGAGGCTCCCTCAAG 448
QY 722 GCGTGCAGTACCTGTCCGCAAGGCTGAGGCGCATGCTTTCTTTCGCAAGAGCAGCCCTTAA 781
DB 449 ACCCTTTTCAAGAACTCACCGGCGCTGA--CCACAGAGTACTGAGCGTGGCCCTTTTGC 506
QY 782 GGAATTTGATGACAGCGCTTCTAAGACAGTTCTGAGAGTGAAGAACTCTTGAGATGCA 841
DB 507 GCACTACCTGAGAGAGATCTTCTTCAACCGTTCCTGCAAGTGAAGTGGCTGGAAGGCA 566
QY 842 ACCAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTGAGGAGAAAGTGTGAGGGA 901
DB 567 GCCAGTACCAAAAACACCTTCAAGCAATACAGAGTCTTGGGTAAAGTGCTTTGGGGA 626
QY 902 GGTATGTGCGCTTCAGGTGAAAAACACTGGAAGATGATGCTGTGAGAAATCTGACAA 961
DB 627 GGTGTGCGCTGTGCAAGGTGCGGCGCACAGGTAAAGTATGCTCGCAAGAACTGAGAA 686
QY 962 GAACGCGCTGAAGAAAGAAAGTGGCGAAGAGTGTCTCTGTGAAAGAAAGAAATCTTGA 1021
DB 687 AAACGCGATTAAGAAAGCGAAAGGAGGCGCATGGGCTGAAGAAACAAATCTGGA 746
QY 1022 GAAGTGCAGAGCCCTTTCATTTCTCTCTGCGCTTATGCTTTGAGAGCAGACCCATCT 1081
DB 747 GAAAGTGAACAGTAAAGTTTGTAGTGAAGCTTGGCTTACGCTTAAAGAACAGAGCGCT 806
QY 1082 CTGCGTGTGATGAGCTGATGAATGGGAGAACTGAAGTCCACATGTACAAAGTGGG 1141
DB 807 GTGCTGTGTGTGACATGATGAACGCGGCGCACTCAAGTTCACATCTCAACATGGG 866
QY 1142 CACGCGTGCCTGACATGAGCGGCGTGAATCTTTTATCTGCGCCACATAGCCTGTGGAGT 1201

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DB 867 CCAGCTGCGCTTCCCGAAGCGCGGCGTCTTCTTACGCGCGAGATCTGTGTGGCT 926
QY 1202 GCTGACCTTCCATGAACTCCGCGATTCGTATATGGAGCATGAACTGTGATGCTTCT 1261
DB 927 GAGAGACCTGACCGGAGCGCATGTGTGACAGGACCTTAACCCGAGAACATCTTGCT 986
QY 1262 GGATGACCTCGCAACTGAGGTTATCTGACTGTGGGCTGGCGGTGAGAGTGAAGGGTGG 1321
DB 987 GGATGACAGCGGCATCCGCATCTCTGACTTGGAGTGTGCTGTGATGTGCCGAGGG 1046
QY 1322 CAAGCCATCACCAGAGGCTGAAACCAATGTTACATGAGTCTCTGAGATCTTAATGA 1381
DB 1047 CCAAGACCATCAAGGCGCTGTGGGACCGTGGGTTCATGAGTCTCGAG--GTGGTGA 1103
QY 1382 AAAAGTAAATGTTATCTTATCTGTGACTGTGGTCCATGGATGCAAGCATTTATGAAT 1441
DB 1104 GAATGAACGCTTCAAGTTCAGCCCTGACTGAGTGGGCGCTGTGCTCTGTACAGAT 1163
QY 1442 GATTGCTGACGAAACACCATTCAAAGATTACAGGAAAGTCAATGAAGAGATCTGAA 1501
DB 1164 GATGAGGCGCATGTGCTCTTCCAGAGAGAAAGATTAAGCGAGAGGAGTGA 1223
QY 1502 GCAAGAACTCTGCAAGACAGAGTCAAAATTCAGCATGATTAATTACAGAGAGCAAA 1561
DB 1224 GCGCTGTGAGAGAGGTCCCGAGAGATTCAGAGCGCTTTCCCGAGGCGCGCTC 1283
QY 1562 AGAATTTGCAAGGCTCTTCTGTGTAAAGAACAGACCAACGTTTGAAGACAGAGAAA 1621
DB 1284 ACTTGTCTACAGCTCTCTGCAAGGACCCGCGAAGCGCTGGGGGTGTCTGTGGGGCAG 1343
QY 1622 GTCTGATGATCCAGAGAAACATCATTTCTTAAAGATCAATTTCTGCGCTGAGAG 1681
DB 1344 TGCCCGGAGGTGAAGAGAGACACCCCTCTTAAAGACTGAACTTCAAGCGGCTGGAGC 1403
QY 1682 TGCGCTAATTAACCCCATTTGTGCAAGACCTTCAGTGTGTTATGCGCAAGACATCCG 1741
DB 1404 TGCGATGTGAGAGCGCGCTTCAAGCTGAGCCCGAGCGCATTTACTCAAGATGTCT 1463
QY 1742 TGAATTTGATATTTCTCTGAGGTTGCGGGGTGAAATTTGATGACAAAGTAAAGCAT 1801
DB 1464 GAGCATTAAGAGTTCCTAAGGTCAAGGCGGTGAGCTGAGCCTACCGACAGAGACTT 1523
QY 1802 CTTCAAAACCTTTCGACAGGTGTGTTCTTATGATGAGAGAGAAATTTATGAAGC 1861
DB 1524 CTACAGAAAGTTTGTCCACAGGAGGTGTCCATGCCCTGTGCAAGAGATGTGAGAC 1583
QY 1862 GGGACTGTTAGGAACTGAATGAC 1886
DB 1584 CGAGTGTCTTCAAGAGCTGAATGTC 1608

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RESULT 10
 US-08-454-439-12
 Sequence 12, Application US/08454439
 Patent No. 5591618
 GENERAL INFORMATION:
 APPLICANT: Chanlry, David
 APPLICANT: Gray, Patrick W.
 APPLICANT: Hoeckstra, Merle F.
 TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSER: Bortun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1758
US-08-454-439-12

Query Match      19.0%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 2.5e-93;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

305 GGGCTTGGACAACTGATGCGCAAGACCGCTTCTGCGCGCGGAAAGCCCTCGGACCTG 364
33 GAGGCTCGAAGACATGTCAGCAACAGGTCCTAATGAGCGCCGGAAGGTGGCGGTGG 92
365 CGACAGCAAAAG--AGCTGACGCGCGCGCGCGCTGAGCTTGGCCCTGCGCGGCTGCAAGG 421
93 AAATGCAAAAGGCAAAAGCAAGAAATGCGCGCGAGATGCTCCAGTTCCTCATCTAGCA 152
422 CTGCGGAGGCTCCGCGCAAGCTGTCCCTGAACTTCCACACCTGTGTGAGAGAGAGC 481
153 GTGCGAAGAGCTGCGGCTCAGCTCGAGCTGATACAGCTGTGTCAGAGCGGACCG 212
482 CATCGGTGCGCGCTCTTCCGTGAGCTTCTAGCAAGTGCAGAGTCCAGAGTCCGCAAGGCGAG 541
213 CATTTGGGCGCTGCTGTTCCGAGAGTTCGTGCAAGAGGCGGAGCTGAGCCGCTGGGT 272
542 AACCTTCTTGAAGACGTGCAAGACTGGAGCTGGCGGAGAGGAGCCCAACCAAGACAG 601
273 CGCTTCTCGTGAATGGGATGCGAGATGAGATGAGTGAACCCGAGATGACAGAGCGAAG 332
602 CGGCTGCAAGGCGCTGTGTCACCTTGTGCAAGTGCCTTCCGCGGAGAAACCGGAGAC 661
333 TGGGCGGCGACG--TAAAGCAAGATTTCTAGGCAAGGAGTCTGATCTCATCTCTGA 389
662 CTTCCTCAAGCGCGCGTGGCGACCAAGTGCAGAGCCACCACTGAGAGAGAGAGT 721
390 GGTTCCTCCGCGAGCTGTGAGCAAC--TGCACCCAGCGGCTGAGAGAGGAGTCCCTGCAAG 448
449 ACCTTTTCAAGGAATTAACCGGCTGA--CCACAGAGTACTGAGGCTGAGCCCTTTTTC 506
722 GGTGCAATGACGCTGCGCAAGGCTGAGGCTGAGCTTTTCTTGAAGAGAGCCCTTTAA 781
782 GGAATTCGTGACAGCGCTTCTTGAAGCAAGTTCCTGAGTGAAGAACTCTTCAAGATGA 841
507 CGACTACTGCAAGCAATCTACTTCAACCGTTCCTTCAAGTGAAGTGGCTGAGAAAGCA 566
842 ACAGGTGTCAGACAGATCTTCACTGATTCAGAGTCTGCGGAGAAAGTGGTCTTTGGGGA 901

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1142 CAGCGTGGCTTGAACATGAGCGCGGTGATCTTTTACTGCGCCAGATAGCTGTGGAT 1201
867 CAGGCTGGCTTCCCGAAGCGCGCGGTCTTCTAGCGCGCGAGATCTGTGGCT 926
1202 GCTGCACTTCCATGAACTCGGCAATGCTATCTGAGGACATGAGAGCTGAGATGCTTCT 1261
927 GAGAGACCTGACCGGAGGCGCATGCTGTACAGGAGCTGAAAGCCGAGAACATCTTGCT 986
1262 GAGTGAACCTGCGCAACCTGAGATGATCTGACCTGGGCTGCGCGTGAAGAGAGTGG 1321
987 GAGTGAACCGGCAACCTGAGATGATCTGACCTGGGCTGCGCGTGAAGAGAGTGG 1046
1322 CAGGCCATCAACCGAGAGGCTGAAACCAATGTTACATGCTCTGAGATCTTAAATGA 1381
1047 CAGAACCATCAAGAGGCTGTGGGACCGTGGGTTACATGCTCTGAGATCTTAAATGA 1103
1382 AAGATTAATTTCTTATCTGATGAGCTGTGGTCCATGAGATGAGATTTAATGA 1441
1104 GAATGAACGTTACAGCTTCAAGCTGAGCTGTGGGCTGTGCTGTGTCAGAT 1163
1442 GTTGTGAGACCAACCATTTCAAGATTTACAGAGAAAGTCAATGAAGATCTGA 1501
1164 GATGAGGCGAGCTGCGCTTCCAGAGAGAGAAAGATTAAGCGGAGAGTGA 1223
1502 GCAAGAACTCTGCAAGAGAGTCAATTTCCAGATGATTAATCTTCAAGAGAGAA 1561
1224 GGGCTGTGAAAGAGATGCCCGAGAGATTTCCAGAGCTTTCCCGCAGCGCTC 1283
1562 AGATATTGAGAGCTCTTCTTGGCTAAGAAACAGAGCAAGCTTGAAGAGAGAA 1621
1284 ACTTGTCTACAGCTTCTTGAAGAGAGCTTGAAGAGAGCTTGAAGAGAGAG 1343
1622 GTTGTGATGATCCAGAGAAACATTTCTTTAAAGATCAACTTTCTGCTGGAAGC 1681
1344 TGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403
1682 TGCGCTAATGAACCCCATTTGTGCAAGAGCTTCAAGTGTGTTAAGCAAGAGATGC 1741
1404 TGCGATCTGAGAGCGGCTTCAAGCTTGAACCCAGAGAGAGAGAGAGAGAGAG 1463
1742 TGAATTAATGAATTTCTGAGAGTGTGGGAGAGAGAGAGAGAGAGAGAGAG 1801
1464 GAGCAATTAAGAGATTTCTTACAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1523
1802 CTTCAGAAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1861
1524 CTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
1862 GGAAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1886
1584 CGAGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1608

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RESULT 11

PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
; PCT-US94-10487-12

Query Match 19.0%; Score 418.2; DB 5; Length 2204;
Best Local Similarity 56.2%; Pred. No. 2.5e-93;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 305 GGCCTTGGAACCTGATCGCAACACCGCTTACTGAGGCGCCGGAGCCCTGAGACTG 364
DB 33 GGAAGCTGGAACATCGTAGCAACAGGTGCTACTCAAGGCCGGGAGAGTGGGGTGG 92
QY 365 CGACAGCAAG--AGCTGAGCGGGGGGGGGTGGAGCTTGGCCCTGCGGCTGCAAGG 421
DB 93 AAATCGCAAGGCAAAAGCAAAAGGAGGAGGAGTGTCTCCAGTCTCCACATCGACCA 152
QY 422 CTGGCGGAGCTTCCGCAAGCTGTCCCTGAATTCACAGGCTGTGTGAGCAGACGCC 481
DB 153 GTGGAGAGAGCTGCGGCTCAAGCTTCGAGGTGATATGACAGCTGTGTGAGCAGCAG 212
QY 482 CATGGTGGCGGCTTCTTCTGATCTTCTTCAAGCAAGTGCACAGTCCAGGTTCCGAGG 541
DB 213 CATGGCGGCTGCTGTTCGAGAGTTCGTGCTCCACAGGCTCGAAGCTGAGCCCTGCT 272
QY 542 AACCTTCTAGAGAGCTGAGAACTGGGAGCTGGCGAGAGAGGAGCCACCAAGAGCAG 601

DB 273 CGCCTTCTGAGATGGGGTGGCCGAGTATGAGTACCOCGGATGACAGCGGAGAGCATG 332
QY 602 CGGCTGCAAGGGGCTGTGACACTTGTGCGAGTCCCTTGGCCCGGGAGACCGCAAC 661
DB 333 TGGGCGGAG--TAAAGCAATTTTCTGAGCCACAGGGTCTCGACATCTCATCTCTGA 389
QY 662 CTTCCTGAGCAGGCGGCTGGCCACCAAGTGGCAAGCCACCACTGAGAGAGAGCATG 721
DB 390 GATCCCCCGGAGCTGTGAGAGAC-TGCACCAGCGCTGAGAGAGGATCTTGCAGAG 448
QY 722 GGTGAGTGAAGCTGCGCAAGGCTGAGGCTTCTTCTGAGAGAGGCTTTAA 781
DB 449 ACCCTTTCCAGAGATCAACCGGCTGA--CCAGAGAGATCTGAGGTGGCCCTTTTGC 506
QY 782 GGAATTCGAGACAGCGCTTCTTACAGCAAGTTCTGATGAGAACTTCTGATGATGA 841
DB 507 CGATCTACTGACAGCACTTACTTCAACGTTTCTGAGTGAAGTGGCTGAGAAAGCA 566
QY 842 ACCAGTGTGAGCAAGTACTTCACTGATGAGTGTCTGGGAGAAAGGTGTTGGGA 901
DB 567 GCGAGTGAACAAAACACTTCAAGGAAACCGAGTCTTGGTAAAGGTGCTTTGGGGA 626
QY 902 GGTATGTGCGTCCAGGTGAAAAACCTGGGAGAGATGTATGCTGTAAAGAACTGACA 961
DB 627 GGTGTGCGCTGCGAGGTGGGCGCACAGGTATAGTATGCTGTGAGAGACTGAGAG 686
QY 962 GAAGCGGCTGAGAAAGAGTGGCGAGAGATGCTCTTGGAAAGAAATCTTGA 1021
DB 687 AAAGCGATCAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 746
QY 1022 GAAGTCAAGAGCCCTTCTTCTGCTCTGCTGCTTCTGAGAGCAAGCCATCT 1081
DB 747 GAAAGTGAACAGTAGTGTGTGATGAGCTTGGCTTAAGCTTATGAGACAGAGAGCGGCT 806
QY 1082 CTGCTTGTATGAGCCTGATGATGAGGAGAGAGCTTCAAGTTCATCAACCTGAG 1141
DB 807 GTGCTGTGTGCTGACACTGATGAGAGGGGGGAGCTCAAGTTCACATCTACATGAG 866
QY 1142 CAGCGTGGCTGAGCACTGAGCGGCTATCTTTTACTGAGCCCGAGATGCTGTGGAT 1201
DB 867 CAGGCTGGCTTCCCGAGAGCGGCGGCTGTCTTACGCGCGAGATCTGTGGCTCT 926
QY 1202 GCTGACCTCCATGAATCTGGGATGCTGATCGGATCATGAGGAGGAGGAGGAGGAG 1261
DB 927 GAGAGACTGACCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 986
QY 1262 GATGACCTGAGCACTGAGGATATCTGACCTGGGCTGGCGGTGAGATGAGAGGAG 1321
DB 987 GATGACAGCGGCAATCGGATCTTGAATCGGAGCTGAGTGTGATGTGCGCGAGG 1046
QY 1322 CAGGCCATCAACAGAGGCTGAGAACCAATGTTATCATGCTCTTGAATCTTAATGA 1381
DB 1047 CAGAGCACTCAAGAGGAGGTGTGGGACCGTGGTTCATGTGCTCGAG--GTGGTGA 1103
QY 1382 AAAGTAAATTAATCTCATCTGTGATCTGATGAGTGTGATGAGGAGGAGGAGGAGGAG 1441
DB 1104 GATTAAGAGTACAGTGTGAGGCTTGAATGTGGGCTGCGCTCTCTGTAAGAGT 1163
QY 1442 GGTGCTGAGCAACCACTTCAAGATTAAGAGAAAGTCAAGTAAAGGATCTGA 1501
DB 1164 GATCCAGAGGAGGAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 1223
QY 1502 GCAAGAACTCTGAGAGAGAGTCAATTCAGCAATGATTAATTCACAGAGAGCAAA 1561
DB 1224 GGGCTGTGAGAGAGTCCCGAGAGAGTATTCGAGGCTTTTCCCGAGGCGCGCTC 1283
QY 1562 AGATATTTGAGAGCTTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1621
DB 1284 ACTTTGCTCAAGAGTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
QY 1622 GTCTGATGATCCAGAGAACTATCTTTCTTAAAGATCAATCTTCTGCTGAGAGC 1681

Db 1344 TGCCCGAGGTGAAGAGACACCCCTCTTTTAAAGAGCTGAATCTGAAGGCTGGAGGC 1403
QY 1682 TGGCTAATTAAGACCCCAATTTGTGCGAAGCCCTTCACTGTTTATGCGAAGACATGCC 1741
Db 1404 TGGCATCTGGAGCCCGCTTCAAGCTGACCCCAAGGCCATTTTACGTGAGAGATGTTCT 1463
QY 1742 TGAATTAAGATTTCTCTGAGGTGGGGGGGTGGGAATTTGATGACAAAGATGACAGTT 1801
Db 1464 GAGACATTAAGACATTTCTTACGCTCAAGGCGTGGAGCTGAGGCTTACGACCAAGACTT 1523
QY 1802 CTTCAAAACCTTTCAGCAGAGTGTCTCTTATAGCATGGCAGGAAATTAATTAAGAAC 1861
Db 1524 CTACCAAGATTTGGCCACAGAGATGTGGCCATCCCTGGAGAAAGAGATGTGAGAAC 1583
QY 1862 GGGACTGTTTGAAGAACTGATGAC 1886
Db 1584 CGAGTCTTCCAGAGCTGATGTC 1608

RESULT 12
US-08-221-817-21
Sequence 21, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoeckstra, Merle P.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
US-08-221-817-21

Query Match 18.0%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 7.9e-88;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

QY 305 GGCCCTGAGCAACTATATGCGCAACCGCCTTACTGAGGCCCGGAAAGCCTCGGATG 364
Db 15 GAGGCTCGAAGAACTGTAGCGAACAAGGCGCTTACGAGCCCGGAGAGTGTGCGG 74
QY 365 CGACAGCAAG--AGTGGAGCGCGCGCGCTGAGCTGCGCCCTGCGCGGTGAGGG 421
Db 75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCGCAATGCTGAGTTTCCCAATCAGCCA 134
QY 422 CTGCGGAGAGCTCGCGCAAGAGCTGCTGAACTTCAACAGCTGTGTGAGCAGAGCC 481
Db 135 GTGTGAAGAGCTCGGCTCACTTGAAGCTGACCTTACAGAGCTGTGTGAGCTGAGTC 194
QY 482 CATCGGTGCGCGCTCTTCCGTGACTCTTACGCAAGTGGCCACGTTTCGCAAGCGCGC 541
Db 195 CATGGAGCGCTGTATTATGTAGATTTGTGCGCTTACGAGGCTGAGCTGAGCCCGTGTAC 254
QY 542 AACCTTCTTAAGAGACGTGCAAACTGGAGCTGGCGGAGAGAGGACCAACCAAGACAG 601
Db 255 TGCCCTTCTGAGTGGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAAGAGAGCATG 314
QY 602 CGGCGTGAAGGGCGTGGTGGCACTTGTGCAAGTGCCTGCGCGCGGAGAACCCGCAACC 661
Db 315 TGGGCGTC--GGCTAATCGAATTTTCTGAGCCACAGGCTCTGACCTCATCCCTGA 371
QY 662 CTTCCTCAAGCAGGCGGTGGCCACCAAGTGCAGAGCCGCACTGAGAAAGCGAGT 721
Db 372 AGTTCCCGGAGCGTGGTGTAGTAC-TGTGCCAGCGGTAGAGCAGGAGACCTGCAAAAG 430
QY 722 GGTGCAAGTACGCTGGCAGCAGGCTGAGGCTGAGCTTGTGCAAGAGAGCCCTTTAA 781
Db 431 ACCCTTTCAGAGAGTACCCGGCTACCCATGATGATCACTAAGCATGAGG--CTTTTGG 488
QY 782 GGAATTCGACACAGCGCTTCTACAGCAAGTTCTGAGTGAATCTTTGAGATGCA 841
Db 489 CGACTTACTGACAGCATCTTCAACCGTTCTCTGAGATGGAAGTGGCTGAAAGGCA 548
QY 842 ACCAGTGTGAGCAAGTACTTCACTGATGTTCAAGTGTGGGAGAAAGTGTGTTGGGGA 901
Db 549 GCGAGTACCAAAAACACTTTAGGAGATGACGAGTCTGGGAGAAAGTGGCTTTGGGGA 608
QY 902 GGTATGTGCGCTGCGAGTGAAGAAACCTGGGAGATGATGCTGTGAAGAACTGAGCA 961
Db 609 GGTGTGTGCTGCGAGTGGCGCAACAGGCAAGTGTATGCTGTACAAAACTGGAAGAA 668
QY 962 GAAGCGCTGAAGAAAGAGTGGCGAGAGATGGCTCTTGGAGAAAGAAATCTTGA 1021
Db 669 GAAACGATTAAGAGCGAGAGGAGGCGCATGTCTCTAAGAGAAAGCATCTTGGAG 728
QY 729 GAAAGTGAACAGTATGATTTGATGATCTTACCTTACGATATGAGCCAGATGACCT 788
QY 1022 GAAAGTCAAGAGCCCTTCACTTCTCTGCGCTATGCTTGAAGAGCAAGCCATCT 1081
Db 729 GAAAGTGAACAGTATGATTTGATGATCTTACCTTACGATATGAGCCAGATGACCT 788
QY 1082 CTGCTTGTATGAGCTGAGTGAAGTGGGGAGACCTGAAGTGCATCTTACAGTGGG 1141
Db 789 GTGCTGTGTGCTGATGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 848
QY 1142 CAAGGTGCTGAGATGAGACCGGAGTATCTTTACTGCGCCAGATGACCTGTGGAT 1201
Db 849 CGAGGCTGCTTTCCGAGAGACGTGTGTGTTCTATGCTGCGAGATCTGTGTGATCT 908
QY 1202 GCTGCACTTCATGAATCGGATATGCTATGAGGACATGAAGCTGAGAAATGTCTTCT 1261
Db 909 GGAAGGACTTACCGGAGAACCATGTGTGATCAGGAGACCTTAAGCGAGAAATATCTTCT 968
QY 1262 GATGATCTCGGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
Db 969 GATGATCTCGGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY 1322 CAAGCCATCAACCAAGAGGCTGAGAACCAATGATGATGATGATGATGATGATGATGAT 1381
Db 1029 CAGACATCAAGAGGCGGTGTGGGACTGTGGGCTAATAGGCTCAAG--GTGGTGA 1085

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QY 1382 AAGTAAATTAATTCCTGCTGAGCTGTTGGCATGGAGCATTTATGAAT 1441
DB 1086 GAATGAGGCGTACACATTCAGTCTGACGTGGGCGCTGCTCTGTCAGAGAT 1145
QY 1442 GGTGCTGAGCAACACATTCAGAGATTAAGAGAAAGGTCAAGAGATCTGAA 1501
DB 1146 GATTGGGAGACGTGCGCTTCCAGCAGAGAGAGAGATCAAGCGGAGAGGTGA 1205
QY 1502 GCAAGAACTGCAAGACAGAGTCAATTCAGCATGATTAATTCAAGAGAGCAAA 1561
DB 1206 GCGGCTGCTCAAGAGAGGTGCTGAGAGATCACAGACCCCTTCCCAAGGCAAGTTC 1265
QY 1562 AGATATTGACAGCTCTTCTGCTGATAGAAACAGAGCAACCTTAAAGAGCAAGAAA 1621
DB 1266 ACTGCTGCTCAAGCTTCTCAACAGAGACCTGCTGAGCGCTGAGGCTGTGAGAGTGG 1325
QY 1622 GTCTGATGATCCAGAAACATCTTCTTAAAGATCACTTCTGCTGAGAGC 1681
DB 1326 TGCCTGAGGTAAAGAGAGACCCCTTTCAGAAACAGATTTCAAGCGCTGAGAGC 1385
QY 1682 TGGCTTAATTAACCCCATTTGTCGACAGACCTTCAAGTGTATGCAAGAGATCGC 1741
DB 1386 TGAATGCTAGAACCACTTTAACTGACCCCAAGCCATTTACTGAGAGAGTGTCT 1445
QY 1742 TGAATGATGATTTCTGAGTTCGAGGCTGAGGAGTGAATTTATGACAAATAGAGT 1801
DB 1446 GAGCATTAACAGTCTTCCAGATTAAGGTGATGATGAGAGCCCAAGACCAAGACTT 1505
QY 1802 CTTCAAAACCTTGCAGACAGTGTCTGCTTCTATAGATGAGAGAAATTAAGAAAC 1861
DB 1506 CTACCAAGAGTTGCCAGCGGTGATGTGCTCATCCCTGAGAGAGAGTGTGAGAGC 1565
QY 1862 GGGACTGTTGAGAGATGAGATGAC 1886
DB 1566 TGAATGCTCAAGAACTAAATGTC 1590

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RESULT 13 US-08-454-439-21

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; Sequence 21, Application US/08454439
; Patent No. 5591618
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle P.
; TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,439
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,817
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5591618and, Greta E.

```

```

; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1740
; US-08-454-439-21

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Query Match 18.0%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 7,9e-88;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

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QY 305 GGCCTGAGCAACTGATTCGCAACACCGCTTACCTGACAGCCCGAAGCCCTGAGACTG 364
DB 15 GAGCTCGAAGACATCGTAGCAACACCGGCGTACTCAAGCCCGGAAGGTGGTGGCG 74
QY 365 CGACAGCAAG---AGCTGACAGCGCGCGGCTAGCTTGGCCCTGCGGAGTGCAGAG 421
DB 75 GAATCTTAAGCAAGAGCAAGAAATGAGCGCAGATCTGCAATTCCTCCCAATCAGCCA 134
QY 422 CTGCGGAGCTCCGCAAGAGCTGCTGTAATTCACAGCTGATGAGAGAGAGAGAGC 481
DB 135 GTGTAAGAGCTCCGCGCTGCTGAGACCTGACCTGATGAGAGAGAGAGAGAGAGT 194
QY 482 CATGCGTCCGCTCTTCCGTAATCTTCTGACAGTCCAGTCCAGTCCGCAAGAGAG 541
DB 195 CATTGGGCGCTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATG 254
QY 542 AACCTTCTTAAGAGAGCTGCAAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
DB 255 TGCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
QY 602 CCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
DB 315 TGGGAGTCT---GGCTAATGAGAAATTTCTGAGCCACAGAGTCTGACTCATCTGTA 371
QY 662 CTTCTCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
DB 372 AGTTCCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
QY 722 GGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
DB 431 ACCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
QY 782 GATTTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
DB 489 CAGTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
QY 842 ACCAGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901
DB 549 GCGAGTGAACAAAACACTTAAGGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
QY 902 GGTATGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
DB 609 GGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
QY 962 GAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
DB 669 GAAAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
QY 1022 GAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
DB 729 GAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788

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QY 782 GGAATTCGAGACGAGGCTTTCAGACAAATTTCTGAGTGAATCTTTCAGATGCA 841
DB CGACTACCTCGACGACATCTACTTCAACGTTTCTGCGAGTGAAGTGGCTGGAAAGGCA 548
QY 842 ACCAGTGTGACAACTACTTCTGAGTTCAGAGTTCGGGGAAGGTTGTTGGGGA 901
DB 549 GCCAGTGAACCAAAAACCTTTTGGGAGTACGAGTCTGGGCAAAAGTGGCTTTGGGGA 608
QY 902 GGTATGTCGCTGCAAGTGTGAAAAACACTGGAGATGATGCTGTAGAAACTGGACA 961
DB 609 GGTGTGTGCTGCTGCGAGGTGGGACAAACAGGAGATGTATGGGTACAAAACTGGAAAA 668
QY 962 GAAGCGGCTGAAAGAAAGGTGGGAGAGATGCTCTTCTGAAAAAGAAATCTTGA 1021
DB 669 GAAACGAATAAAGAAAGGAGAGGAGGAGGAGGATGCTCTCAACGAGAGAGATCTGGA 728
QY 1022 GAAGTCAAGACGCTTTCATTTGCTCTGCGGCTGAGCTTTCAGAGCAAGACCATCT 1081
DB 729 GAAAGTGAACAGTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 788
QY 1082 CTGCTGTGATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141
DB 789 GTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 1142 CAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1201
DB 849 CAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 908
QY 1202 GCTGACCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1261
DB 909 GAGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 968
QY 1262 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
DB 969 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY 1322 CAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1381
DB 1029 CAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
QY 1382 AAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441
DB 1086 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
QY 1442 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1501
DB 1146 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1205
QY 1502 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1561
DB 1206 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1265
QY 1562 AAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1621
DB 1266 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325
QY 1622 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1681
DB 1326 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
QY 1682 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1741
DB 1386 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1445
QY 1742 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1801
DB 1446 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1505
QY 1802 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1861
DB 1506 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565

QY 1862 GGAAGCTGTTGAGGAACTGAATGAC 1886
DB 1566 TGAGTGTCTTCAGGAACTAATATGC 1590

RESULT 15
US-08-221-817-10
Sequence 10, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Boston
STREET: 6300 Seare Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1926
US-08-221-817-10

Query Match 17.7%; Score 389.4; DB 1; Length 2206;
Best Local Similarity 55.3%; Pred. No. 3.1e-96;
Matches 866; Conservative 0; Mismatches 681; Indels 18; Gaps 5;

QY 305 GGCCTGAGCAACCTGATGCGCAACACGCTTACCTGACAGCCCGAAGCCCTGAGACTG 364
DB 33 GAGAGCTCGAGAACTGTAAGCAACGAGTGTCTACTCAAGGCCCGGAAAGGTGGCGGTG 92
QY 365 CGACAGCAAG--AGTGTGAGCGCGCGCGCGAGTGTCTTCAAGTCTTCTCAACAGCA 421
DB 93 AATTCGCAAGGCAAAAGCAAGAAATGCGGCGAGATGCTTCAAGTCTTCTCAACAGCA 152
QY 422 CTGCGGAGCTCGCGAGAGCTGTCTTGAATCTTCAACAGCTGTGTGAGAGAGGCG 481
DB 153 GTGCGAAGAGCTGTGCGCTGAGCTGAGCTGAGCTTCAACAGCTGTGTGAGAGAGGCG 212
QY 482 CAGCGTGTGCGCTTCTGAGCTTCTTCAAGCAAGTGTGCGCAAGTGTGCGCAAGGCGCG 541

1	2198	100.0	2198	7	AB557315	Ab557315 CDNA encorr
2	2008.8	91.4	2249	4	AAH78799	Aah78799 Human G-F
3	1988.8	90.5	3186	7	ACC44827	Acc44827 Human G-F
4	1817.8	82.7	1821	9	ADCC9221	Adcc9221 Novel human
5	1817.8	80.0	1761	7	ABZ65943	Abz65943 Human gene
6	1658.8	75.5	1662	6	ABQ86118	Abq86118 Novel human
7	1658.8	75.5	1662	6	AAD26466	Aad26466 Human cDNA
8	1658.8	75.5	1662	6	AAD63530	Aad63530 Human cor
9	1658.4	75.5	1662	4	AAH78797	Aah78797 Human G-F
10	1657.2	75.4	1662	4	AAD8071	Aad8071 Human Kif
11	1655.6	75.3	1662	4	AA506702	Aas06702 Polynucleid
12	1655.6	75.3	1662	7	ACCA4826	Acc44826 Human G F
13	1615.7	54.0	1191	7	ABZ56934	Abz56934 Human RGE
14	1470.4	53.2	1486	6	AAD65351	Aad65351 Human cor
15	1046.8	47.6	1062	4	AAH78798	Aah78798 Human G-F
16	867.4	39.5	3651	6	AAD28072	Aad28072 Human Kif
17	419.6	19.1	2848	4	AAH24842	Aah24842 Human Kif
18	418.2	19.0	2204	4	AAO87426	Aah7426 Human GRK
19	418.2	19.0	2848	6	ABL61805	AbL61805 Colon adenoc
20	418.2	19.0	2848	6	ABR49405	AbR49405 CDNA encorr
21	403.8	18.4	2541	9	ADBS3307	Ads3307 Primary r
22	395.8	18.0	1983	2	AAO87427	Aag7427 Rat GRK C
23	389.4	17.7	2206	2	AAO87425	Aag7425 Human GRK

PT disorders.

XX

Db	1741	CTGAATATGATATTTCTCTGAGGTTGGGGGAGTGGAAATTGATGCAAAAGATAGAGT	1800
Qy	1801	TCCTCAAAACCTTTGGCAGCAGTGCTGTCTCTTACATGCGCAGAGAAATTATGAAA	1860
Db	1801	TCCTCAAAACCTTTGGCAGCAGTGCTGTCTCTTACATGCGCAGAGAAATTATGAAA	1860
Qy	1861	CGGAGCTGTTTASGAAGCTGAATGACCCCAACAGACTAGGGGTGTGAGAGGGTAAAT	1920
Db	1861	CGGAGCTGTTTASGAAGCTGAATGACCCCAACAGACTAGGGGTGTGAGAGGGTAAAT	1920
Qy	1921	CATCCAAAGCTGGGGGTGTGTTGTAATGTAAATGTCTCTTTACACAGCAGGCACAG	1980
Db	1921	CATCCAAAGCTGGGGGTGTGTTGTAATGTAAATGTCTCTTTACACAGCAGGCACAG	1980
Qy	1981	GAGTCTCGGCTGACATATCTCGAATGTTCACACGTGGAAATCTGTGGAATAGAGGCT	2040
Db	1981	GAGTCTCGGCTGACATATCTCGAATGTTCACACGTGGAAATCTGTGGAATAGAGGCT	2040
Qy	2041	AATCAGTGGAGGGGACATCACAACACAAACAAATTGAAAAGCAGGACAGCTCACATAC	2100
Db	2041	AATCAGTGGAGGGGACATCACAACACAAACAAATTGAAAAGCAGGACAGCTCACATAC	2100
Qy	2101	TAGAACACATTTATTTCTTTTCTTCTCTAATAAGTAGAAGCTCAGTTTCA	2160
Db	2101	TAGAACACATTTATTTCTTTTCTTCTCTAATAAGTAGAAGCTCAGTTTCA	2160
Qy	2161	CTGAGGCGAGGAAAAGAAACACTAGGTTATTTTGA	2198
Db	2161	CTGAGGCGAGGAAAAGAAACACTAGGTTATTTTGA	2198

CC derived from the nucleotides of the invention are useful as hybridisation
CC probes for screening libraries and assessing gene expression patterns.
CC The nucleotides of the invention are also useful in drug screening and
CC gene therapy for the modulation of GRK expression. The nucleotides of the
CC invention can be used to genetically engineer host cells to express GRK
CC products *in vivo*. The nucleotide sequences of the invention are also
CC useful in addressable arrays for identifying and characterising the
CC temporal and tissue specific expression of a gene and in microarrays to
CC screen collections of genetic material from patients who have a
CC particular medical condition. The proteins of the invention are useful
CC for generating antibodies, as reagents in diagnostic assays, for
CC identifying other cellular gene products related to GRK, and as reagents
CC in assays for screening for compounds that are useful in the treatment of
CC mental, biological or medical disorders/diseases
XX
XX Sequence 2249 BP, 582 A, 577 C, 608 G, 482 T, 0 U, 0 Other;

CC	AAH78799	standard; cDNA; 2249 BP.
AC	AAH78799;	
DT	08-MAR-2002	(first entry)
XX		
DE	Human G-protein coupled receptor kinase 3 cDNA sequence.	
XX		
KM	G-protein coupled receptor kinase; GRK; human; ss; gene therapy;	
KM	drug screening; gene expression characterisation; NRP;	
KM	novel human protein.	
XX		
OS	Homo sapiens.	
XX		
PM	M0200168869-A2.	
PD	20-SEP-2001.	
XX		
PF	08-MAR-2001; 2001MO-US007500.	
XX		
PR	10-MAR-2000; 2000US-0188449P.	
XX		
PA	(LEXI-) LEXICON GENETICS INC.	
XX		
PI	Walke DM, Milgadowski NL, Turner CA;	
XX		
DR	WPI; 2001-570872/64.	
XX		
PT	New polynucleotides encoding human proteins that share sequence	
PT	similarity with animal kinases e.g. G-protein coupled receptor kinases	
PT	useful for drug screening, diagnosis and in gene therapy of biological	
XX	disorders.	
XX		
PS	Disclosure; Page 33-34; 34pp; English.	
XX		
CC	The present cDNA sequence encodes a human G-protein coupled receptor	
CC	kinase (GKR), also designated NRP (novel human protein) in the	
CC	specification, which is shown in the sequence listing. The invention	
CC	comprises novel human nucleotide and protein sequences which have	
CC	similarity to G-protein coupled receptor kinases. Oligonucleotides	

CC acid sequences that encode the GRK enzyme
XX Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;

Query Match 90.5%; Score 1988.8; DB 7; Length 3186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 207 CGTTGCTCAACCCGGAAGGAAAGAGCAGCAGCCCTTCAGCCCTTTGTGCTTCC 266
DB 1 CGTTGCTCAACCCGGAAGGAAAGAGCAGCAGCCCTTCAGCCCTTTGTGCTTCC 60
QY 267 TGGAGTGGCCCGCTGCTGACGACATGATGAGCATGGGGGCGCTGACACCTGATGCGC 326
DB 61 TGGAGTGGCCCGCTGCTGACGACATGATGAGCATGGGGGCGCTGACACCTGATGCGC 120
QY 327 AACACGCTCACTTGGAGAGCCCGGAAGCCCTGAGCATGGAGCAAGAGCTTCAGCCG 386
DB 121 AACACGCTCACTTGGAGAGCCCGGAAGCCCTGAGCATGGAGCAAGAGCTTCAGCCG 180
QY 387 CGGCGGCTGAGCTGAGCCCTGCGCGGAGCTGAGGAGCTGCGGAGAGCTCCGCGAAGCTG 446
DB 181 CGGCGGCTGAGCTGAGCCCTGCGCGGAGCTGAGGAGCTGCGGAGAGCTCCGCGAAGCTG 240
QY 447 TCCCTGAATCTTCAACGCTGCTGTGAGAGAGCCCATGCGCTGCTTCCGTGAC 506
DB 241 TCCCTGAATCTTCAACGCTGCTGTGAGAGAGCCCATGCGCTGCTTCCGTGAC 300
QY 507 TTCTTGAACAGAGTGGCCAGTTCGAGAGAGCCGAACTTCTTGAAGAGTTCAGAAC 566
DB 301 TTCTTGAACAGAGTGGCCAGTTCGAGAGAGCCGAACTTCTTGAAGAGTTCAGAAC 360
QY 567 TGGAGCTGGCCGAGAGAGAGCCCAAAAGAGAGCGCTGAGGAGCTGATGAGCACT 626
DB 361 TGGAGCTGGCCGAGAGAGAGCCCAAAAGAGAGCGCTGAGGAGCTGATGAGCACT 420
QY 627 TGTGAGAGTGGCCCTGCGCGGAGAACCCGGAACCTTCTTCAAGCAGAGCTGTGAC 686
DB 421 TGTGAGAGTGGCCCTGCGCGGAGAACCCGGAACCTTCTTCAAGCAGAGCTGTGAC 480
QY 687 AAGTGCAGAGAGAGCAGCAGTGAAGAGAGAGAGTGGTGGAGTGGTGGAGAGT 746
DB 481 AAGTGCAGAGAGAGCAGCAGTGAAGAGAGAGAGTGGTGGAGTGGTGGAGAGT 540
QY 747 GAGGCCATGCTTCTTCAAGAGAGAGCCCTTTAAGATTTGTGACAGAGCTTCAAC 806
DB 541 GAGGCCATGCTTCTTCAAGAGAGAGCCCTTTAAGATTTGTGACAGAGCTTCAAC 600
QY 807 GACAGATTTCTGAGTGAAGAACTTTCAGATGACACAGTGTGACAGAGTACT 866
DB 601 GACAGATTTCTGAGTGAAGAACTTTCAGATGACACAGTGTGACAGAGTACT 660
QY 867 GAGTTGAGAGTGGTGGGAAAGGTGTTTGGGAGAGTATGAGTGGTGGAGTGAAGAA 926
DB 661 GAGTTGAGAGTGGTGGGAAAGGTGTTTGGGAGAGTATGAGTGGTGGAGTGAAGAA 720
QY 927 ACTGGAAGATGATGCTGTGTAAGAACTGAGACAGAGCGCTGAGAGAGAGTGGC 986
DB 721 ACTGGAAGATGATGCTGTGTAAGAACTGAGACAGAGCGCTGAGAGAGAGTGGC 780
QY 987 GAGAGATGGCTCTCTTGAAGAAAGAAATCTTGAAGAGTGAAGAGCCCTTCAATGTC 1046
DB 781 GAGAGATGGCTCTCTTGAAGAAAGAAATCTTGAAGAGTGAAGAGCCCTTCAATGTC 840
QY 1047 TCTTGGGCTATGCTTCTTGAAGAGAGAGCCATCTGCTGCTGATGAGAGCTGAGAT 1106
DB 841 TCTTGGGCTATGCTTCTTGAAGAGAGAGCCATCTGCTGCTGATGAGAGCTGAGAT 900
QY 1107 GGGGAGAGCTCAAGTTCAATCTTCAAGAGTGGAGACGCTGCTGAGCATGAGCCG 1166
DB 901 GGGGAGAGCTCAAGTTCAATCTTCAAGAGTGGAGACGCTGCTGAGCATGAGCCG 960
QY 1167 GTGATCTTTTACTGGCCGAGATAGCTGTGGAGTGTGACCTTCATGAACTGGCATC 1226
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DB 961 GTGATCTTTTACTGGCCGAGATAGCTGTGGAGTGTGACCTTCATGAACTGGCATC 1020
QY 1227 GTGATGGGAGCATGAGACCTGAGAAATGCTTCTTGAATGACCTTGGCAATCTGAGTGA 1286
DB 1021 GTGATGGGAGCATGAGACCTGAGAAATGCTTCTTGAATGACCTTGGCAATCTGAGTGA 1080
QY 1287 TCTGACCTGGGAGCTGGCGCTGAGATGAGAGAGTGGCAAGCCCATCACCCAGAGGCTGGA 1346
DB 1081 TCTGACCTGGGAGCTGGCGCTGAGATGAGAGAGTGGCAAGCCCATCACCCAGAGGCTGGA 1140
QY 1347 ACCAATGTTTACATGCTCTTCAAGATCTTAATGAGAAAGTAAAGTATCTTATCTGTG 1406
DB 1141 ACCAATGTTTACATGCTCTTCAAGATCTTAATGAGAAAGTAAAGTATCTTATCTGTG 1200
QY 1407 GACTGTTTCCATGGAGATGACGATTTATGAATGTTGTGAGAGAACCATTTCAA 1466
DB 1201 GACTGTTTCCATGGAGATGACGATTTATGAATGTTGTGAGAGAACCATTTCAA 1260
QY 1467 GATTACAGAGAAAGGTGATGTAAGAGATCTGAAGCAAGAACTGCGAAGAGGTC 1526
DB 1261 GATTACAGAGAAAGGTGATGTAAGAGATCTGAAGCAAGAACTGCGAAGAGGTC 1320
QY 1527 AAATTCAGATGATTAATCTTCAAGAGAGAGAAAGATTTTGAAGCTCTTCTTGGCT 1586
DB 1321 AAATTCAGATGATTAATCTTCAAGAGAGAGAAAGATTTTGAAGCTCTTCTTGGCT 1380
QY 1587 AAGAAACAGAGAGACGCTTGAAGAGAGAGAAAGCTGTATGATCCAGAAACATCAT 1646
DB 1381 AAGAAACAGAGAGACGCTTGAAGAGAGAGAAAGCTGTATGATCCAGAAACATCAT 1440
QY 1647 TTCTTTAAACGATCACTTCTCTGCTGAGAGCTGAGCTGAATTAACCCCATTTGTG 1706
DB 1441 TTCTTTAAACGATCACTTCTCTGCTGAGAGCTGAGCTGAATTAACCCCATTTGTG 1500
QY 1707 CCAAGCCCTTCAAGTGTATTAAGCAAGACATCGCTGAATTAATTAATCTTCTGAGGTT 1766
DB 1501 CCAAGCCCTTCAAGTGTATTAAGCAAGACATCGCTGAATTAATTAATCTTCTGAGGTT 1560
QY 1767 CGGGGGTGGAAATTTGATGACAAAGATTAAGAGCTTCTTCAAAACCTTTCGAGAGTCT 1826
DB 1561 CGGGGGTGGAAATTTGATGACAAAGATTAAGAGCTTCTTCAAAACCTTTCGAGAGTCT 1620
QY 1827 GTTCTTATAGCATGAGAGAGAAATTTATAGAAAGGAGCTGTTTGAAGAACTGAATGAC 1886
DB 1621 GTTCTTATAGCATGAGAGAGAAATTTATAGAAAGGAGCTGTTTGAAGAACTGAATGAC 1680
QY 1887 CCAACAGACCTTACGAGTGTGAGAGAGGTTAATTCATCAAGTCTGGCTGTGTTGTA 1946
DB 1681 CCAACAGACCTTACGAGTGTGAGAGAGGTTAATTCATCAAGTCTGGCTGTGTTGTA 1740
QY 1947 TTGTAATTTGCTCTCTTTTACAGAGAGAGAGAGTCTGGCTGACATTAATCTGGAA 2006
DB 1741 TTGTAATTTGCTCTCTTTTACAGAGAGAGAGAGTCTGGCTGACATTAATCTGGAA 1800
QY 2007 TGTTCACAGTGAAGATCTGAGAAATGAGGCTTAATCAAGTGAAGAGGAGCATCAAC 2066
DB 1801 TGTTCACAGTGAAGATCTGAGAAATGAGGCTTAATCAAGTGAAGAGGAGCATCAAC 1860
QY 2067 ACAAAACATTAAGAGAGAGAGCTCACTAAGAGACATTAATTTCTTTTCT 2126
DB 1861 ACAAAACATTAAGAGAGAGAGCTCACTAAGAGACATTAATTTCTTTTCT 1920
QY 2127 TTCTTCAATTAAGATGAGAAAGTCTGATTTCACTGAGGAGGAGAAAGAACTCA 2186
DB 1921 TTCTTCAATTAAGATGAGAAAGTCTGATTTCACTGAGGAGGAGAAAGAACTCA 1980
QY 2187 GATTATTTTGA 2198
DB 1981 GATTATTTTGA 1992
```

RESULT 4

Db		1201	AGATTACAAAGAAAAGGTCAGTAAAGAAGATCTGAAGCAAGAAACTTGCGAAGCAGAGGT	1260
Oy		1526	CAAATTCACGATGATTAATCTTCAGAGGGAGAACAAAGATTTATTTAGAGCTCTTCTGGCC	1585
Db		1261	CAAAATTCACGATGATTAATCTTCAGAGGGAGAACAAAGATTTATTTAGAGCTCTTCTGGCC	1320
Oy		1586	TAAAGAACACGACGACAGCTTGAGNACAGAGAAAGTCTGATGATCCGAGAAACATCA	1645
Db		1331	TAAAGAACACGACGACAGCTTGAGNACAGAGAAAGTCTGATGATCCGAGAAACATCA	1380
Oy		1646	TTTCTTTAAAAAGCATCACTTTCCTGCCTGGAAGCTGGCCTTAATTGAACCCCATTTGT	1705
Db		1381	TTTCTTTAAAAAGCATCACTTTCCTGCCTGGAAGCTGGCCTTAATTGAACCCCATTTGT	1440
Oy		1706	GCGAGACCCTTCAGTGGTTTATGCCAAGACATGCGCTGAAATTTGATGATTTCTGAGGT	1765
Db		1441	GCGAGACCCTTCAGTGGTTTATGCCAAGACATGCGCTGAAATTTGATGATTTCTGAGGT	1500
Oy		1766	TGCGGGGGGTGAAATTGATGACAAGATAAGCATTTCTTCAAAAACCTTGTGCGACAGGTGC	1825
Db		1501	TGCGGGGGGTGAAATTGATGACAAGATAAGCATTTCTTCAAAAACCTTGTGCGACAGGTGC	1560
Oy		1826	TGTTCTATAGCATGCGCAGAGAAAGAAATTATGAAAACGAGACTGTTTGAGAACTGAATGA	1885
Db		1561	TGTTCTATAGCATGCGCAGAGAAAGAAATTATGAAAACGAGACTGTTTGAGAACTGAATGA	1620
Oy		1886	CCCCAACAGACCTTACGGGTTTGAGAGAGGGTAAATTCACCAACTGCGAGGTGTTTGGT	1945
Db		1621	CCCCAACAGACCTTACGGGTTTGAGAGAGGGTAAATTCACCAACTGCGAGGTGTTTGGT	1680
Oy		1946	ATTGTAAATTCCTCTCTTTACACAGCACGACAGAGAGTCTCGGCTGACATATACCTCGA	2005
Db		1681	ATTGTAAATTCCTCTCTTTACACAGCACGACAGAGAGTCTCGGCTGACATATACCTCGA	1740
Oy		2006	ATGTTCCACACGTGGAATCT 2026	
Db		1741	ATGTTCCACACGTGGAATCT 1761	
RESULT 6				
ABQ86178				
ID	ABQ86178	standard; DNA; 1662 BP.		
AC	XX	ABQ86178;		
XX	XX	10-SEP-2002 (first entry)		
DT	DE	Novel human gene. SEQ ID 49.		
XX	XX			
KM	KM	Human; cytostatic; vulnery; antiarteriosclerotic; antiparkinsonian;		
KM	KM	nootropic; neuroprotective; immunosuppressive; haemostatic;		
KM	KM	antiinflammatory; cardiant; antidiuretic; vitamin; antithyroid;		
KM	KM	cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;		
KM	KM	wound healing disorders; arteriosclerosis; Parkinson's disease;		
KM	KM	Alzheimer's disease; autoimmune disorder; haematopoietic disorder;		
KM	KM	inflammation; neoplastic disease; nervous system disorder;		
KM	KM	cardiovascular disorders; pancreatitis; respiratory disorder;		
KM	KM	hyperproliferation; systemic autoimmune disease; hyper-immunity;		
KM	KM	developmental abnormality; gastrointestinal ulceration; neuropathy;		
KM	KM	haematological disease; metabolic diseases; sperm dysfunction;		
KM	KM	thyroid disorder; hypothyroidism; brain damage; colitis;		
KM	KM	angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;		
KM	KM	tractus; thymus; lymph node; muscular system; obesity; anorexia;		
XX	OS	growth abnormality; precocious puberty; gene; ss.		
XX	OS	Homo sapiens.		
XX	PN	WO200250105-A1.		
XX	PD	27-JUN-2002.		
PF		17-DEC-2001; 2001MO-US049232.		

XX 19-DEC-2000; 2000US-0256710P.
PR 20-DEC-2000; 2000US-0257048P.
PR 09-JAN-2001; 2001US-0260482P.
PR 30-JAN-2001; 2001US-0264922P.
PR 06-FEB-2001; 2001US-0266797P.
PR 19-MAR-2001; 2001US-0276988P.
PR 04-APR-2001; 2001US-0281535P.
PR 08-MAY-2001; 2001US-0289622P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Birkeland M, Cogswell JP, Kahnuk KF, Lai Y;
PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX MPI. 2002-508784/54.
XX P-85DB, ABP61013.
XX
XX Secreted proteins and polynucleotides useful as vaccines for preventing
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS Claim 2(a); Page 255-256; 335pp; English.

XX The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cytoprotective, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardiant, antitumor, virucide, antihypertensive, cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmune disorder, haemopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder,
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiodysplasia,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in records ABQ66130-ABQ66184 represent novel human cDNA's
CC of the invention
XX
SQ Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Query Match 75.5%; Score 1658.8; DB 6; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGGACATGAGGAGGCTGAGCAACCTGATCCCAACCGCTTACCTGACAGCGCCG 350
DB 1 ATGTGGACATGAGGAGGCTGAGCAACCTGATCCCAACCGCTTACCTGACAGCGCCG 60
QY 351 AAGCCCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGAC 410
DB 61 AAGCCCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCTGGAC 120
QY 411 GGGCTGCAAGGCTGCGAGAGCTCGCAGAAAGCTGCTCCCTGAACTTCCACAGCTGGT 470
DB 121 GGGCTGCAAGGCTGCGAGAGCTCGCAGAAAGCTGCTCCCTGAACTTCCACAGCTGGT 180
QY 471 GAGCAGCAGCCATCGTGGCTGCTCTTCCGTAATCTTCAAGCAAGTCCAGCTTC 530
DB 181 GAGCAGCAGCCATCGTGGCTGCTCTTCCGTAATCTTCAAGCAAGTCCAGCTTC 240
QY 531 CGAAGGCGGCACTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 590

DB 241 CGCAAGGCGCAACCTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 300
QY 591 ACCAAGAAGCAGCGCTGAGAGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGG 650
DB 301 ACCAAGAAGCAGCGCTGAGAGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGG 360
QY 651 AACCCGCAACCTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 710
DB 361 AACCCGCAACCTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 420
QY 711 GAAAGAGAGTGGCTGAGTGAAGCTGCGCAAGCTGAGGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 770
DB 421 GAAAGAGAGTGGCTGAGTGAAGCTGCGCAAGCTGAGGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 480
QY 771 CAGGCTTTAAGATTTGGTGAACAGGCTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAG 830
DB 481 CAGGCTTTAAGATTTGGTGAACAGGCTTCTTCAAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAG 540
QY 831 TTGAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGGTGGAGAAAGT 890
DB 541 TTGAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAGAGTGGTGGAGAAAGT 600
QY 891 GGTTTGGAGAGGTATGTGCTGCTGAGTGAAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 950
DB 601 GGTTTGGAGAGGTATGTGCTGCTGAGTGAAGCACTGGAGCACTGGAGCACTGGAGCACTGGAG 660
QY 951 AAATGCAACAGAGCGCTGAGAGAAAGTGGAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAG 1010
DB 661 AAATGCAACAGAGCGCTGAGAGAAAGTGGAGCAAGTGGAGCACTGGAGCACTGGAGCACTGGAG 720
QY 1011 GAAATCTTGGAGAGGTGAGAGGCTTTCATTTCTCTGAGCTTATGCTTTGAGAGC 1070
DB 721 GAAATCTTGGAGAGGTGAGAGGCTTTCATTTCTCTGAGCTTATGCTTTGAGAGC 780
QY 1071 AAGACCATCTTCTGCTTGTATGAGCTGATGAATGGAGAGCACTGATTCATTCATC 1130
DB 781 AAGACCATCTTCTGCTTGTATGAGCTGATGAATGGAGAGCACTGATTCATTCATC 840
QY 1131 TAGAAGTGGAGCGAGGCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1190
DB 841 TAGAAGTGGAGCGAGGCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 900
QY 1191 GCTTGGAGATGCTGACCTGATGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1250
DB 901 GCTTGGAGATGCTGACCTGATGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 960
QY 1251 AATGTCTTGTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1310
DB 961 AATGTCTTGTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1020
QY 1311 ATGAAGGAGGAGAGCCATACCCAGAGAGGCTGGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1370
DB 1021 ATGAAGGAGGAGAGCCATACCCAGAGAGGCTGGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1080
QY 1371 ATCTTAATGAGAAAGTAAATTTCTTATCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1430
DB 1081 ATCTTAATGAGAAAGTAAATTTCTTATCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1140
QY 1431 ATTATTAATGAGTGTGCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1490
DB 1141 ATTATTAATGAGTGTGCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1200
QY 1491 GAGGATGAGAGCAAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1550
DB 1201 GAGGATGAGAGCAAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1260
QY 1551 GAGGAGCAAGAAATATTTGAGAGCTTTCTTGTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1610
DB 1261 GAGGAGCAAGAAATATTTGAGAGCTTTCTTGTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAG 1320
QY 1611 AGCAGAGAAATCTGATGATCCAGAGAAATCTTCTTAAACATTAATCTTCTTCTTCTTCTTCTTCTTCTTCT 1670
DB 1321 AGCAGAGAAATCTGATGATCCAGAGAAATCTTCTTAAACATTAATCTTCTTCTTCTTCTTCTTCTTCTTCT 1380

QY 1671 CGCTGGAAGCGGCTTAATTGAACCCATTGTGTGCAGACCTTCAGTGGTTTATGCC 1730
 DB 1381 CGCTGGAAGCGGCTTAATTGAACCCATTGTGTGCAGACCTTCAGTGGTTTATGCC 1440
 QY 1731 AAGACATCGCTGAATATGATGATTTCTCTGAGGGGTGGAATTTGATGACAA 1790
 DB 1441 AAGACATCGCTGAATATGATGATTTCTCTGAGGGGTGGAATTTGATGACAA 1500
 QY 1791 GATAGCAGTTCTTCAAAAACCTTGGCAGAGTCTCTTCTATAGCATGCGAGAA 1850
 DB 1501 GATAGCAGTTCTTCAAAAACCTTGGCAGAGTCTCTTCTATAGCATGCGAGAA 1560
 QY 1851 ATATAGGAAGCGGACGTTTGGAGAACGTAATGACCCCAAGACCTACGGGTGTGAG 1910
 DB 1561 ATATAGGAAGCGGACGTTTGGAGAACGTAATGACCCCAAGACCTACGGGTGTGAG 1620
 QY 1911 GAGGTATATTCATCAAGTCTGCGTGTGTTTATTTATTA 1952
 DB 1621 GAGGTATATTCATCAAGTCTGCGTGTGTTTATTTATTA 1662

RESULT 7
 AAD26466 standard; cDNA; 1662 BP.
 XX AAD26466;
 AC AAD26466;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human kinase PKIN-19 cDNA.
 XX
 KW Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis;
 KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
 KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
 KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
 KW fatty liver; Niemann-Pick's disease; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag=a
 FT /product="Human PKIN-19 protein"
 XX
 PN W0200196547-A2
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US019444.
 XX
 PR 15-JUN-2000; 2000US-0212073P.
 PR 23-JUN-2000; 2000US-0213467P.
 PR 30-JUN-2000; 2000US-021651P.
 PR 07-JUL-2000; 2000US-021665P.
 PR 13-JUL-2000; 2000US-0218372P.
 PR 25-AUG-2000; 2000US-0228056P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
 PI Gandhi AR, Tribouley CW, Walla NK, Yao MG, Lu DM, Greenwald SR,
 PI Ramtamer J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT,
 PI Baughman MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R,
 PI Lo TP, Khan F, Reippon SA, Azimtai Y, Policky DJ, Ding L,
 PI Grether W, Elliott VS, Thangavelu K, Bacteria S, Ison CH;

DR WP1; 2002-090207/12.
 DR P-PSDB; AAE16273.
 XX
 FT New polypeptides, useful for diagnosing, treating or preventing disorders
 FT of growth and development, cardiovascular and lipid, and diseases such as
 FT cancer, comprise human kinase polypeptides.
 PS
 XX
 PS Claim 5, Page 190; 197pp; English.
 CC The invention relates to human kinase PKIN proteins and their
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for
 CC treating a disease or condition associated with decreased expression of
 CC PKIN and a composition comprising PKIN antagonist is useful for treating
 CC a disease or condition associated with overexpression of PKIN. The
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 CC of a test compound and in gene therapy. The present sequence is human
 CC PKIN-19 cDNA
 CC
 XX
 S0 Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 Query Match 75.5%; Score 1658.8; DB 6; Length 1662;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 291 ATGGTGACATGGGGGCGCTGACAACTGATGCGCAACCGCTACCGGACCGG 350
 DB 1 ATGGTGACATGGGGGCGCTGACAACTGATGCGCAACCGCTACCGGACCGG 60
 QY 351 AAGCCTCGGACTGCGACGCAAGAGCTGCGCGCGCGGTAGCCTGCGCCTGCC 410
 DB 61 AAGCCTCGGACTGCGACGCAAGAGCTGCGCGCGCGGTAGCCTGCGCCTGCC 120
 QY 411 GGGCTGCAAGGGCTGCGGAGCTCGCGAGAGCTGCTCTGAACTTCCACAGCTGTGT 470
 DB 121 GGGCTGCAAGGGCTGCGGAGCTCGCGAGAGCTGCTCTGAACTTCCACAGCTGTGT 180
 QY 471 GAGCAGCAGCGCATGCGGTGCGCGCTCTTCGCTGACTTCAGCGCAGTGCAGCTT 530
 DB 181 GAGCAGCAGCGCATGCGGTGCGCGCTCTTCGCTGACTTCAGCGCAGTGCAGCTT 240
 QY 531 CGCAGAGCGGCAACTTCTAGAGAGCTGCGAGAACTGCGAGCTGCGCGAGAGAGCC 590
 DB 241 CGCAGAGCGGCAACTTCTAGAGAGCTGCGAGAACTGCGAGCTGCGCGAGAGAGCC 300
 QY 591 ACCAAAGACGCGGTGCGAGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 650
 DB 301 ACCAAAGACGCGGTGCGAGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 360
 QY 651 AACCGGACCGCTTCTGAGCAGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 710
 DB 361 AACCGGACCGCTTCTGAGCAGCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 420
 QY 711 GAAAGCAGATGCTGCGATGAGAGCTGCGAGAGCTGCGAGAGCTGCGATGCTTCTG 770
 DB 421 GAAAGCAGATGCTGCGATGAGAGCTGCGAGAGCTGCGAGAGCTGCGATGCTTCTG 480
 QY 771 GAGCCTTTAAGATTTTGATACCAAGGCTTCTGACAGATTTCTGACAGGAACTC 830

Db 481 CAGCCCTTAAGSATTTCGACAGCGCCTTACAGCAAGTTCTGCACTGAAACTC 540
 QY 831 TTGAGATGCAACCAAGTGTGACCAAGTATCTTCACTGAGTGTGAGGAAAGT 890
 Db 541 TTGAGATGCAACCAAGTGTGACCAAGTATCTTCACTGAGTGTGAGGAAAGT 600
 QY 891 GGTTTGGGAGGATATGCGCCGACGGTGAAGAAACCTGGAAGATATGCTGTAG 950
 Db 601 GGTTTGGGAGGATATGCGCCGACGGTGAAGAAACCTGGAAGATATGCTGTAG 660
 QY 951 AAATGGAACAAGACGGCTGAAGAAAGAGTGGGAGAAATGGCTCTCTTGGAAAG 1010
 Db 661 AAATGGAACAAGACGGCTGAAGAAAGAGTGGGAGAAATGGCTCTCTTGGAAAG 720
 QY 1011 GAATCTTGAGAAAGTCAAGACCCCTTCACTGCTGCTGCTGCTGCTTGAAGC 1070
 Db 721 GAATCTTGAGAAAGTCAAGACCCCTTCACTGCTGCTGCTGCTGCTTGAAGC 780
 QY 1071 AAGACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
 Db 781 AAGACCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 1131 TACAAGTGGGACAGCGTGGCTGACATGAGCGGGTGAATCTTTTACTGGGCCAGTA 1190
 Db 841 TACAAGTGGGACAGCGTGGCTGACATGAGCGGGTGAATCTTTTACTGGGCCAGTA 900
 QY 1191 GCTGTGGATGCTGACCTCCATGAACTCGGATCGTCTATCGGACATGAAAGCTGAG 1250
 Db 901 GCTGTGGATGCTGACCTCCATGAACTCGGATCGTCTATCGGACATGAAAGCTGAG 960
 QY 1251 AATGTCTTCTGGAATACCTCGGCACTGCAAGGTATCTGACTGCGGGCTGCGCTGAG 1310
 Db 961 AATGTCTTCTGGAATACCTCGGCACTGCAAGGTATCTGACTGCGGGCTGCGCTGAG 1020
 QY 1311 ATGAAGGTGGCAAGCCCATCAACCAAGGGCTGGAACCAAGGTATCAAGCTCTCTAG 1370
 Db 1021 ATGAAGGTGGCAAGCCCATCAACCAAGGGCTGGAACCAAGGTATCAAGCTCTCTAG 1080
 QY 1371 ATCTTAATGAAAAGTAAATCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1430
 Db 1081 ATCTTAATGAAAAGTAAATCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1431 ATTATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1490
 Db 1141 ATTATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 1491 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTGAATTCGACGATGATCTTCA 1550
 Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGAGGTGAATTCGACGATGATCTTCA 1260
 QY 1551 GAGGAGCAAGAAATATTTGCAAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
 Db 1261 GAGGAGCAAGAAATATTTGCAAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 QY 1611 AACCAAGAAAGTGTGATGATCCGAGAAACATCATTTCTTAAACGATCAACTTCT 1670
 Db 1321 AACCAAGAAAGTGTGATGATCCGAGAAACATCATTTCTTAAACGATCAACTTCT 1380
 QY 1671 CCGCTGAAGCTGGCCCTAATGAAACCCCAATTTGGCCAGACCCCTGAGGTGATAGC 1730
 Db 1381 CCGCTGAAGCTGGCCCTAATGAAACCCCAATTTGGCCAGACCCCTGAGGTGATAGC 1440
 QY 1731 AAAAGCATCGTGAATATGATATTTCTGAGTTCGAGGAGTGAATTTGATGACAA 1790
 Db 1441 AAAAGCATCGTGAATATGATATTTCTGAGTTCGAGGAGTGAATTTGATGACAA 1500
 QY 1791 GATAGCACTTCTTCAAAACCTTTGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1850
 Db 1501 GATAGCACTTCTTCAAAACCTTTGCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 QY 1851 ATTATGAAACGGGACCTGTTGAGGAGCTGAATGACCCCAAGACCTGAGGTTGTAG 1910
 Db 1561 ATTATGAAACGGGACCTGTTGAGGAGCTGAATGACCCCAAGACCTGAGGTTGTAG 1620

QY 1911 GAGGTAATTCATCCAGTCTGAGTGTGTTGTTATTTGTA 1952
 Db 1621 GAGGTAATTCATCCAGTCTGAGTGTGTTGTTATTTGTA 1662
 RESULT 8
 AAD46350
 ID AAD46350 standard; cDNA; 1662 BP.
 AC AAD46350;
 DT 27-JAN-2003 (first entry)
 XX Human cone opsin kinase (GRK7) cDNA.
 DE Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW microbiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1..1662
 FT CDS /tag= a
 FT /product= "Human GRK7 protein"
 FT
 PN MO200272541-A2.
 PD 19-SEP-2002.
 PE 07-MAR-2002; 2002MO-US007025.
 PR 07-MAR-2001; 2001US-0274006P.
 PA (IMMW) IMMUNEX CORP.
 PI Bird TA, Spencer M, Mosley BA;
 XX WPI; 2002-72307/78.
 DR P-PSDB; AAE28952.
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual
 PT signalling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4; Page 45-46; 61pp; English.
 XX
 CC The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signalling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC blindness), pineal gland activity (e.g., microbiological desynchrony,
 CC depression, anxiety, mental foginess, memory loss, headaches, fatigue,
 CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
 CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
 CC preparation of a medicament for treating a condition or disease related
 CC to cone photoreceptor visual signalling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for

CC individuals with such disorders. The present sequence is human GRK7 cDNA
XX
SQ Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Query Match	75.5%	Score 1658.8	DB 6	Length 1662
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1660; Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy	291	ATGTGTGAATATGSGGGGCGCTGGACAACCTGATATGCGCAACACCGCTCAACTGTCAGAGCGCG	350
Db	1	ATGTGTGAATATGSGGGGCGCTGGACAACCTGATATGCGCAACACCGCTCAACTGTCAGAGCGCG	60
Qy	351	AAAGCCTCTGGACTGCGACAGCAAAAGAGCTGCAGCGCGCGCGGTAGGCTGTGCGCTTGGCC	410
Db	61	AAAGCCTCTGGACTGCGACAGCAAAAGAGCTGCAGCGCGCGCGGTAGGCTGTGCGCTTGGCC	120
Qy	411	GGGCTGCAAGGCTGTGCGGAGGCTTCGCGCAAGAGCTGTCTCTGAACCTTCCAGACGCTGTGT	470
Db	121	GGGCTGCAAGGCTGTGCGGAGGCTTCGCGCAAGAGCTGTCTCTGAACCTTCCAGACGCTGTGT	180
Qy	471	GAGAGCACACCCCATCGAGTGCACGCGCTCTTCCGTGACCTTCTAGACCAAGTGCACAGTTC	530
Db	181	GAGAGCACACCCCATCGAGTGCACGCGCTCTTCCGTGACCTTCTAGACCAAGTGCACAGTTC	240
Qy	531	CGCAAGCGCGCAACTTCTCTAGAGGAGCGTGCAGAACTGAGAGCTGAGCTGCGAGAGGAGCC	590
Db	241	CGCAAGCGCGCAACTTCTCTAGAGGAGCGTGCAGAACTGAGAGCTGAGAGCTGCGAGAGGAGCC	300
Qy	591	ACCAAAAGACAGCGGCTGCGAGGGGCTGGTGGCCACTTGTGTGGAGTACCCCTGCGCGGGG	650
Db	301	ACCAAAAGACAGCGGCTGCGAGGGGCTGGTGGCCACTTGTGTGGAGTACCCCTGCGCGGGG	360
Qy	651	AAACCCGAAACCTTCTCTCAGCGAGCGCGTGGGACCAAGATGCGCAAGACCAACACTGTAG	710
Db	361	AAACCCGAAACCTTCTCTCAGCGAGCGCGTGGGACCAAGATGCGCAAGACCAACACTGTAG	420
Qy	711	GAAAGCGAGTGGCTGCGAGTGAAGCTGTGGCGAAGGCTGAGGACACTGTGCTTTCTTGCAGAG	770
Db	421	GAAAGCGAGTGGCTGCGAGTGAAGCTGTGGCGAAGGCTGAGGACACTGTGCTTTCTTGCAGAG	480
Qy	771	CAGGCTTTAAGATTTGCTGACACAGGCGCTTCTACAGATTTGTGGAGTGGAGAAC	830
Db	481	CAGGCTTTAAGATTTGCTGACACAGGCGCTTCTACAGATTTGTGGAGTGGAGAAC	540
Qy	831	TTGAGATGCAACAGAGTGCAGACAAAGTACTTCACTGAGTTCAAGATGCTGCGAGAAAGT	890
Db	541	TTGAGATGCAACAGAGTGCAGACAAAGTACTTCACTGAGTTCAAGATGCTGCGAGAAAGT	600
Qy	891	GATTTTGGGAGGTATGTGCGGTCCAGGTGAAAACCTGGAGAAATGATATGCTGTAGAG	950
Db	601	GATTTTGGGAGGTATGTGCGGTCCAGGTGAAAACCTGGAGAAATGATATGCTGTAGAG	660
Qy	951	AAATCGGACAAAGACGCGCTGAAGAAAGAGTGGCGAGAAATGAGCTCTTGTGAAAAG	1010
Db	661	AAATCGGACAAAGACGCGCTGAAGAAAGAGTGGCGAGAAATGAGCTCTTGTGAAAAG	720
Qy	1011	GAATCTTGGAGAGGTCAAGACGCCCTTTCAATGTCTCTCTGAGCTATGCTCTTGAAGC	1070
Db	721	GAATCTTGGAGAGGTCAAGACGCCCTTTCAATGTCTCTCTGAGCTATGCTCTTGAAGC	780
Qy	1071	AAAGCCATCTTGTGCTTTGATGAGCTTGATGATATGGGAGAGCTTCAAGTGCACATTC	1130
Db	781	AAAGCCATCTTGTGCTTTGATGAGCTTGATGATATGGGAGAGCTTCAAGTGCACATTC	840
Qy	1131	TTCAACGTGGGAGACGCGTGGGCTGAGACATGACGCGGAGTATCTTTACTCGGCGCAATAT	1190
Db	841	TTCAACGTGGGAGACGCGTGGGCTGAGACATGACGCGGAGTATCTTTACTCGGCGCAATAT	900
Qy	1191	GCTGTGGGATCTGCACTTCATGAACTTGGCATGTCTTATCGGACATGAAAGCTGAG	1250
Db	901	GCTGTGGGATCTGCACTTCATGAACTTGGCATGTCTTATCGGACATGAAAGCTGAG	960
Qy	1251	AAATGTCTTCTGGATGACCTTGGCAACTGCAAGGTATCTGACCTTGGGCGTGGCGTGGAG	1310

Dd		961	AATGTCTTCCTTGGATTACCTCGGCAACTGGAAGTTAATGTACCCTTGCGGCCTGGCGTAGG	1020
Oy		1311	ATGAAAGGCTGGCAAGCCCATCACCAGAAGGCTGSAAACAATGTTTAATGCTGCTTGAG	1370
Dd		1021	ATAAAGGCTGGCAAAGGCCCATCACCCAGAAGGCTGSAAACAATGTTTAATGCTGCTTGAG	1080
Oy		1371	ATCTTAATGAAAAAGGTAAGTTATTCATATCCCMGNGASCTGGTTTTGCCATGGAGTAGCAG	1430
Dd		1081	ATCTTAATGAAAAAGGTAAGTTATTCATATCCCMGNGASCTGGTTTTGCCATGGAGTAGCAG	1140
Oy		1431	ATTATATGAATAGTGTCTGSGAAGAACCACTTCAAGATTAACAAGAAAAGSTCAATAAA	1490
Dd		1141	ATTATATGAATAGTGTCTGSGAAGAACCACTTCAAGATTAACAAGAAAAGSTCAATAAA	1200
Oy		1491	GAGGATCTGAAGCAAAAGAACTCTGCAAGACAGAGTGCAAAATTCAGCATGTATACCTTACA	1550
Dd		1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGACAGAGTGCAAAATTCAGCATGTATACCTTACA	1260
Oy		1551	GAGGAGCAAAAGATATTTTGACAGCTCTCTTGCGCTTAAGAAACACAGCAAGGTTAGAA	1610
Dd		1261	GAGGAGCAAAAGATATTTTGACAGCTCTCTTGCGCTTAAGAAACACAGCAAGGTTAGAA	1320
Oy		1611	AGCAGAGAAAAGTGTGATGATCCAGAGAAACATCATTTCTTTAAAAGATCACTTTCT	1670
Dd		1321	AGCAGAGAAAAGTGTGATGATCCAGAGAAACATCATTTCTTTAAAAGATCACTTTCT	1380
Oy		1671	CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCAAGACCTTCAGTGTTTATGCC	1730
Dd		1381	CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCAAGACCTTCAGTGTTTATGCC	1440
Oy		1731	AAAGACATGCTGTAATAATGATGATTTCTCTGAGAGTTCGGGGGGGTGAATTTGATGACAA	1790
Dd		1441	AAAGACATGCTGTAATAATGATGATTTCTCTGAGAGTTCGGGGGGGTGAATTTGATGACAA	1500
Oy		1791	GATPACAGTCTCTTCAAAAAATTTGCGACAGGTGCTGTTCCTATAGCATGACAGAAAGA	1850
Dd		1501	GATPACAGTCTCTTCAAAAAATTTGCGACAGGTGCTGTTCCTATAGCATGACAGAAAGA	1560
Oy		1851	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCACAAGACTTACGGGTTGTGAG	1910
Dd		1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCACAAGACTTACGGGTTGTGAG	1620
Oy		1911	GAGGTAATTGATCCAAGTCTGGCGTGTGTTCCTATATTGTAA	1952
Dd		1621	GAGGTAATTGATCCAAGTCTGGCGTGTGTTCCTATATTGTAA	1662
RESULT 9				
AAH78797				
ID	AAH78797	standard;	CDNA; 1662 BP.	
XX AC	AAH78797;			
XX DT	08-MAR-2002	(first entry)		
XX DD				
XX DX	Human G-protein coupled receptor kinase 1 cDNA sequence.			
KM KM	G-protein coupled receptor kinase; GRK; human; ss; gene therapy;			
KW KW	drug screening; gene expression characterisation; NRP;			
KX KM	novel human protein.			
OS XX	Homo sapiens.			
FH PH	Key	Location/Qualifiers		
FT FT	CDS	1..1662	/+tag= a	
PD PD		/product= "G-protein coupled receptor kinase 1"		
XX XX	WO200168869-A2.			
XX PD	20-SEP-2001.			

Db 1501 GATAGACGTTCTTCAAAAACCTTTCGACAGTGTCTTCTATAGATGAGGAGAA 1560
 QY 1851 ATTATAGAAAACGAGCTGTTTGAAGAACTGATGACCCCAACAGACTTACGGTGTAG 1910
 Db 1561 ATTATAGAAAACGAGCTGTTTGAAGAACTGATGACCCCAACAGACTTACGGTGTAG 1620
 QY 1911 GAGGTAATTCATGCAAGCTGCGGCTGTGTTTGTATGTA 1952
 Db 1621 GAGGTAATTCATGCAAGCTGCGGCTGTGTTTGTATGTA 1662

RESULT 10
 AAD28071
 ID AAD28071 standard; cDNA; 1662 BP.
 XX AAD28071;
 XX 22-APR-2002 (first entry)
 XX Human kinase cDNA.
 XX Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
 KW chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1.1662
 FT /*tag= a
 FT /product= "Human kinase protein"
 XX
 XX W020192496-A2.
 XX 06-DEC-2001.
 XX 31-MAY-2001; 2001WO-US017510.
 XX 01-JUN-2000; 2000US-0208311P.
 PR 18-DEC-2000; 2000US-00738894.
 XX (APPL-) APPLERA CORP.
 PA
 PI Guegler K, Di Francesco V, Beasley EM;
 DR WPI: 2002-130533/17.
 DR P-PSDB; AAE17136.
 XX New isolated human kinase proteins and nucleic acids, useful as a major
 PT target for drug action and development, particularly for screening
 PT modulators of the kinase peptides.
 XX
 PS Claim 4; Fig 1; 87pp; English.
 XX
 XX The invention relates to human kinase proteins that are related to G-
 CC protein coupled receptor kinase subfamily. Human kinase gene is located
 CC on chromosome 3. The kinase peptide and nucleic acid are useful in the
 CC development of human therapeutic and diagnostic compositions. The peptide
 CC is useful as a major target for drug action and development, and is
 CC valuable to the field of pharmaceutical development to identify and
 CC characterize modulators of the kinase. The proteins may also be used to
 CC raise antibodies or to elicit an immune response, as a reagent in assays
 CC designed to quantitatively determine levels of the protein in biological
 CC fluids and as markers for tissues in which the corresponding protein is
 CC preferentially expressed (either constitutively or at a particular stage
 CC of tissue differentiation or development or in a disease state). The
 CC kinase proteins are also useful for providing a target for diagnosing a
 CC disease or predisposition to disease mediated by the peptide. The nucleic
 CC acid molecules are useful for probes, primers, chemical intermediates and
 CC in biological assays. The nucleic acids are also useful in making vectors
 CC containing the gene regulatory regions of the nucleic acid molecules and
 CC for drug screening to identify compounds that modulate kinase nucleic
 CC acid expression. The present sequence is human kinase cDNA expressed in
 CC skins, germinal center B cells, colon, kidney and lung

XX
 SQ Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;
 Query Match 75.4%; Score 1657.2; DB 6; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGGTGAACATGGGGGCGCTGAGCAACCTGATCGCCCAACCGCTTACCTGAGGCCG 350
 Db 1 ATGGTGAACATGGGGGCGCTGAGCAACCTGATCGCCCAACCGCTTACCTGAGGCCG 60

QY 351 AAGCCCTGAGCTGAGACAGCAAAAGCTGACGCGCGCGGCTAGCTTGGCTTGGCC 410
 Db 61 AAGCCCTGAGCTGAGACAGCAAAAGCTGACGCGCGCGGCTAGCTTGGCTTGGCC 120

QY 411 GGGTGTGAGGCTGTGGGGAGCTCCGCCGAAAGCTGTCCCTGAACCTTCCAGCTGTGT 470
 Db 121 GGGTGTGAGGCTGTGGGGAGCTCCGCCGAAAGCTGTCCCTGAACCTTCCAGCTGTGT 180

QY 471 GAGCAGACCCCATGGTGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTCCCACTTC 530
 Db 181 GAGCAGACCCCATGGTGTGCGCGCTCTTCCGTGACTTCTAGCCACAGTCCCACTTC 240

QY 531 CGCAAGCGGCAACCTTCTTGAAGACGTGCAAACTGGGAGCTTGGCCGAGAGGACCC 590
 Db 241 CGCAAGCGGCAACCTTCTTGAAGACGTGCAAACTGGGAGCTTGGCCGAGAGGACCC 300

QY 591 ACCAAAGACAGCGCGCTGCAAGGGGCTGTGGCACTTGTGCGAGTCCCTGGCCCGGG 650
 Db 301 ACCAAAGACAGCGCGCTGCAAGGGGCTGTGGCACTTGTGCGAGTCCCTGGCCCGGG 360

QY 651 AACCCGCAACCTTCTCTACAGCCAGGCGGTGGCCACAGTGTCCCAAGCCACCACTGAG 710
 Db 361 AACCCGCAACCTTCTCTACAGCCAGGCGGTGGCCACAGTGTCCCAAGCCACCACTGAG 420

QY 711 GAAGAGGAGTGGCTGCAAGTACGCTTGGCCCAAGGCTGAGGCTTCTTCTCAAGAG 770
 Db 421 GAAGAGGAGTGGCTGCAAGTACGCTTGGCCCAAGGCTGAGGCTTCTTCTCAAGAG 480

QY 771 CAGCCCTTTAAGATTTGTGACCAAGGCTTCTTCAAGCAAGTTTGTGAGTGAATCTC 830
 Db 481 CAGCCCTTTAAGATTTGTGACCAAGGCTTCTTCAAGCAAGTTTGTGAGTGAATCTC 540

QY 831 TTCGAGATGCAACGATGTGACCAAGTACTTCACTGATGTTGAGTGTGCGGGAAGGT 890
 Db 541 TTCGAGATGCAACGATGTGACCAAGTACTTCACTGATGTTGAGTGTGCGGGAAGGT 600

QY 891 GCTTTGGGAGGTATGTGCGCTGTCAGGTGAATAACACTGGGAAGTGTATGCTGTAG 950
 Db 601 GCTTTGGGAGGTATGTGCGCTGTCAGGTGAATAACACTGGGAAGTGTATGCTGTAG 660

QY 951 AAATGGAACAAGCGGCTGGAAGAAAGGTGCGGAAGTGTGCTCTTGGAAAG 1010
 Db 661 AAATGGAACAAGCGGCTGGAAGAAAGGTGCGGAAGTGTGCTCTTGGAAAG 720

QY 1011 GAAATCTTGAAGAGTCAAGAGCCCTTCAATGTCTCTGCTGACTATGCTTGAAGC 1070
 Db 721 GAAATCTTGAAGAGTCAAGAGCCCTTCAATGTCTCTGCTGACTATGCTTGAAGC 780

QY 1071 AAGACCATTTGCTGCTGTATGAGCCTTGAAGATGGGGGAGACCTCAAGTCCACATC 1130
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QY 1131 TACAAGTGGGACGCGTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 1190
 Db 841 TACAAGTGGGACGCGTGGCTGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 900

QY 1191 GCTGTGGATGTGCACTTCATGAACTCGGCATGTGTATGCGGACATGAAGCTGAG 1250
 Db 901 GCTGTGGATGTGCACTTCATGAACTCGGCATGTGTATGCGGACATGAAGCTGAG 960

QY 1251 AATGTGCTTGTGATGACTTGGCAATGTGAGTTATCTGACTTGGGGCGGCGGTGAG 1310

XX Novel disease-associated gene of the RGS gene family and its product.
 PT applicable in diagnosis of and screening for drugs for heart diseases,
 PT cancers and omentopathy.
 XX
 PS Claim 6; Page 81-82; 96pp; Japanese.
 XX
 CC The invention relates to a novel disease associated gene and its uses.
 CC The gene and its encoded protein are useful for diagnosis of and
 CC screening for drugs for heart diseases, cancers and omentopathy. The
 CC current sequence represents the human RGS99 encoding DNA sequence
 XX
 SQ Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;
 Query Match 54.0%; Score 1187.8; DB 7; Length 1191;
 Best Local Similarity 99.8%; Pred. No. 6,3e-297;
 Matches 1189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGGTGAACATGGGGGCTGTGACCAACCTGATCCCAACACGCTTACTGACAGCCCG 350
 Db 1 ATGGTGAACATGGGGGCTGTGACCAACCTGATCCCAACACGCTTACTGACAGCCCG 60

QY 351 AAGCCTCGGACTGCGACAGCAAAAGAGCTGACGCGCGCGGTGAGCTGGCTGGCC 410
 Db 61 AAGCCTCGGACTGCGACAGCAAAAGAGCTGACGCGCGGTGAGCTGGCTGGCC 120

QY 411 GGGCTGACAGGGCTGGGGAGCTCGCGCAAGAGCTGTCCTGAACTGCAAGCTGTGT 470
 Db 121 GGGCTGACAGGGCTGGGGAGCTCGCGCAAGAGCTGTCCTGAACTGCAAGCTGTGT 180

QY 471 GAGCAGACAGCCCATCGGTCCCGCTCTTCCGTGACTTCTTACGACAGTSCCAAGTTC 530
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QY 531 CGCAAGCGCGCAACCTTCTCTAGAGAGCTGCAAGAGCTGCAAGAGTGGCAAGAGAGCC 590
 Db 241 CGCAAGCGCGCAACCTTCTCTAGAGAGCTGCAAGAGTGGCAAGAGTGGCAAGAGAGCC 300

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 Db 301 ACCAAGACAGGGGCTGCGAGGGGCTGAGGCGCACTTGTGCAAGAGCCCGCGCGGG 360

QY 651 AACCGCAACCTTCTCTAGAGAGCTGCGAGGGGCTGCAAGAGTGGCAAGAGAGCCACTGAG 710
 Db 361 AACCGCAACCTTCTCTAGAGAGCTGCGAGGGGCTGCAAGAGTGGCAAGAGAGCCACTGAG 420

QY 711 GAAGAGCGAGTGGCTGCGAGTGAAGCTGCGCAAGGCTGAGGCACTTCTTGGCAAGG 770
 Db 421 GAAGAGCGAGTGGCTGCGAGTGAAGCTGCGCAAGGCTGAGGCACTTCTTGGCAAGG 480

QY 771 CAGCCTTTAAGAGATTGCTGACAGGCGCTTCTAGAGCAAGTTCTGCGAGTGGAAATC 830
 Db 481 CAGCCTTTAAGAGATTGCTGACAGGCGCTTCTAGAGCAAGTTCTGCGAGTGGAAATC 540

QY 831 TTGAGATGCAACAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGT 890
 Db 541 TTGAGATGCAACAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGT 600

QY 891 GGTGGGGAGAGTGTGCGCTTCAAGTGAAGAAACCTGCGAAGAGTATGCTTGAAG 950
 Db 601 GGTGGGGAGAGTGTGCGCTTCAAGTGAAGAAACCTGCGAAGAGTATGCTTGAAG 660

QY 951 AAATGCAAGAGAGCGGCTGAAAGAAAGGTGGCGAGAGAGTGGCTCTTGGAAAG 1010
 Db 661 AAATGCAAGAGAGCGGCTGAAAGAAAGGTGGCGAGAGAGTGGCTCTTGGAAAG 720

QY 1011 GAAATCTTGAAGAGGTGACAGAGCCCTTCAATGCTCTCTGAGCTTATGCTTGAAGC 1070
 Db 721 GAAATCTTGAAGAGGTGACAGAGCCCTTCAATGCTCTCTGAGCTTATGCTTGAAGC 780

QY 1071 AAGACCATCTCTGCTTGTGATGAGCTGATGAATGGGGGAGAGCTTCAAGTCCAGTC 1130
 Db 781 AAGACCATCTCTGCTTGTGATGAGCTGATGAATGGGGGAGAGCTTCAAGTCCAGTC 840

QY 1131 TACAACTGGGGCAAGGCTGCTGCAATGAGCCGGGATCTTTTACTGGCCAGATA 1190
 Db 841 TACAACTGGGGCAAGGCTGCTGCAATGAGCCGGGATCTTTTACTGGCCAGATA 900

QY 1191 GCTGTGGAGATGCTGACCTCCATGAATCTCGGATCTGTATCGGACATGAAGCTGAG 1250
 Db 901 GCTGTGGAGATGCTGACCTCCATGAATCTCGGATCTGTATCGGACATGAAGCTGAG 960

QY 1251 AATGTCTTCTGATGACCTTGGCACTGCAAGTATCTGACTGGGGCTGGCCGTGAG 1310
 Db 961 AATGTCTTCTGATGACCTTGGCACTGCAAGTATCTGACTGGGGCTGGCCGTGAG 1020

QY 1311 ATGAAGGGTGGCAAGCCATCAACCCAGAGGGCTGGAACCAATGTTATCATGCTCTGAG 1370
 Db 1021 ATGAAGGGTGGCAAGCCATCAACCCAGAGGGCTGGAACCAATGTTATCATGCTCTGAG 1080

QY 1371 ATCTAATGGAAGAGTAAGTATCTTATCTGTGACTGGTTGGCATGGAGTGCAGC 1430
 Db 1081 ATCTAATGGAAGAGTAAGTATCTTATCTGTGACTGGTTGGCATGGAGTGCAGC 1140

QY 1431 ATTATGAATGTTGCTGAGACGAACCAATTCATGAAGATTCAGAGAAAG 1491
 Db 1141 ATTATGAATGTTGCTGAGACGAACCAATTCATGAAGATTCAGAGAAAG 1191

RESULT 14
 AAD46351
 ID AAD46351 standard; cDNA, 1486 BP.
 AC AAD46351;
 XX
 AC AAD46351;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
 XX
 KW Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW chromobiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 1..1062
 FT /*tag= a
 FT /product= "Human GRK7 OK6 splice variant protein"
 XX
 XX NC020272541-A2.
 XX
 PD 19-SEP-2002.
 XX
 PD 07-MAR-2002; 2002MO-US007025.
 XX
 PF 07-MAR-2001; 2001US-0274006P.
 XX
 PR (IMMUNEX CORP.
 XX
 PA Bird TA, Spencer M, Mosley BA;
 XX
 PI Bird TA, Spencer M, Mosley BA;
 XX
 DR WPI: 2002-723307/78.
 DR
 DR P-PSDB; AAE28953.
 XX
 XX
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual
 PT signaling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4; Page 48-49; 61pp; English.
 XX
 CC The present invention relates to novel human cone opsin kinase (G-protein

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 10:30:45 ; Search time 5722.66 Seconds

(without alignments)
16647.489 Million cell updates/sec

Title: US-10-044-205A-1

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Gapop 10.0 ; Gapept 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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1: gb_ba:*

2: gb_hrg:*

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21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hrg_hum:*

31: em_hrg_inv:*

32: em_hrg_other:*

33: em_hrg_mus:*

34: em_hrg_pln:*

35: em_hrg_rod:*

36: em_hrg_nam:*

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41: em_hrgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	2198	100.0	2198	6	AX797552
2	2008.8	91.4	2249	6	AR225819
3	2008.8	91.4	2249	6	AX252443
4	1988.8	90.5	3186	6	AX710216
5	1988.8	90.5	3186	6	AF282269
6	1795.8	81.7	1799	9	AF439409
7	1757.8	80.0	1761	6	BD186115
8	1659	75.5	1659	6	AX797554
9	1658.8	75.5	1662	6	AX797554
10	1658.4	75.5	1662	6	AX642968
11	1658.4	75.5	1662	6	AR225817
12	1657.2	75.4	1662	6	AX252439
13	1657.2	75.4	1662	6	AR263766
14	1657.2	75.4	1662	6	AR343544
15	1655.6	75.3	1662	6	AX357902
16	1655.6	75.3	1662	6	AX166511
17	1640.8	74.6	1701	6	AX710213
18	1422.2	64.7	2453	6	AF282270
19	1404	63.9	2420	4	AY049726
20	1225	55.7	3095	10	AF063016
21	1187.8	54.0	1191	6	BD186106
22	1046.8	47.6	1062	6	AR225818
23	1046.8	47.6	1062	6	AX252441
24	867.4	39.5	36651	6	AR263767
25	867.4	39.5	36651	6	AR343545
26	867.4	39.5	36651	6	AX357904
27	867.4	39.5	125041	2	AC068693
28	867.4	39.5	215077	9	AC112504
29	586	26.7	125041	2	AC068693
30	572.4	26.0	2898	5	AB055658
31	553	25.2	2954	5	AB009568
32	425.6	19.4	2898	4	BOVRKXIN
33	425.6	19.3	2105	9	BC017272
34	423	19.2	1789	9	AF040752
35	423	19.2	2632	9	AF040751
36	423	19.2	2708	9	BC009277
37	419.8	19.1	2848	6	AR160365
38	418.8	19.1	2549	9	U00686
39	418.2	19.0	2204	6	I23378
40	418.2	19.0	2204	6	I33280
41	418.2	19.0	2848	6	AX329633
42	418.2	19.0	2848	9	HUMPROCRI
43	411.8	18.7	2145	9	AK056697
44	409.6	18.6	1952	10	AF040749
45	409.6	18.6	1997	10	AF040747

ALIGNMENTS

RESULT 1

AX797552 2198 bp DNA PAT 04-OCT-2003

LOCUS AX797552

DEFINITION Sequence 1 from Patent WO02095032.

ACCESSION AX797552

VERSION AX797552.1 GI:37518055

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUthors Kapeller-Ribermann, R. and Bandaru, R.

Method and compositions of human proteins and uses thereof

JOURNAL Patent: WO 02095032-A1 28-NOV-2002;

Db	1798	ACATCGCTGAATTTGATGATTTCTCTGTAGGGTTTGGGGGGGTGGAAATTTGATGACAAAGATA	1857
Qy	1795	AGCAGTCTTTCAGAAAATTTCGCGACAGAGTCTGCTTTCTATAGATGCGAGAGAAATTA	1854
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Db	1918	TAGAAAACGGGACTGTTTGAGGAACTGAATGATCCCAACAGACTAAGGGTGTGAGAGG	1977
Qy	1915	GTATATCATCCAACTCTGGGCTGTCTTTGTATGTAAATGCTCTTTTACAGACAGG	1974
Db	1978	GTATATCATCCAACTCTGGGCTGTCTTTGTATGTAAATGCTCTTTTACAGACAGG	2037
Qy	1975	CACGAGAACTCTCGCGCTGACATATCCCGAATGTTCCACGCGGAATCTGGGAATG	2034
Db	2038	CACGAGAACTCTCGCGCTGACATATCCCGAATGTTCCACGCGGAATCTGGGAATG	2097
Qy	2035	AGGGCTATACAGTTAGAGGSGACATCAACAACAAACAAATTCAAAAGACAGGCAACT	2094
Db	2098	AGGGCTATACAGTTAGAGGSGACATCAACAACAACAAATTCAAAAGACAGGCAACT	2157
Qy	2095	CACACTAGAACACATTTTATTTTCTTTTCTTTCTTTCAATAAGATGAGTAAAGTCTCAG	2154
Db	2158	CACACTAGAACACATTTTATTTTCTTTTCTTTCTTTCAATAAGATGAGTAAAGTCTCAG	2217
Qy	2155	TTTTCACTAGGGGACAGGAAAGAAAGAACACTCA	2186
Db	2218	TTTTCACTAGGGGACAGGAAAGAAAGAACACTCA	2249

RESULT 3	AX252443	LOCUS	AX252443	2249 bp	DNA	linear	PAT 05-OCT-2001
DEFINITION	Sequence	5	from Patent WO0168869.				
ACCESSION	AX252443						
VERSION	AX252443.1		GI:15985735				

REFERENCE	1
AUTHORS	Walke, D.W., Wilganowski, N.L. and Turner, C.A.
TITLE	Human g-coupled protein receptor kinases and polynucleotidases encoding the same
JOURNAL	Patent: WO 0168869-A 5 20-SHP-2001;
FEATURES	Lexicon Genetics Incorporated (US)
SOURCE	Location/Qualifiers 1..2249

ORIGIN

	Query Match	91.4%:	Score 2008.8;	DB 6;	Length 2249;
	Best Local Similarity	99.9%:	Pred. No. 0;		
	Matches 2010;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps	0;
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QY	235	CCAGCAGCCCTCAGCCCTCTTGTGTCTTCCCTGGAGATGCGCCCGTGTCTCAGCCATG	294		
DB	298	CCACACGCCCTCAGCCCTCTTGTGTCTTCCCTGGAGATGCGCCCGTGTCTCAGCCATG	357		
QY	295	TGGACATGGGGGGCCCTGGACAACTGATCGCAACAACGCCCTACCTGACAGGCCGGAAGC	354		
DB	358	TGGACATGGGGGGCCCTGGACAACTGATCGCAACAACGCCCTACCTGACAGGCCGGAAGC	417		
QY	355	CCTCGACCTGCGACAGCAAGAAGCTGACAGCGGCGGCGTGAAGCTTGGCCCTGGCGC	414		

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OY	415	TGCAAGGCTGCGCGAGAGCTTCGCGCAAGCTGTCTCTGAACTTCCAAGCTGTGTGAGC	474
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OY	535	AGGCGGCAACCTTCTTAGAGAGACTGTGAGCACTGGAGAGCTGGCCAGAGAGGAAACCAACA	594
Db	598	AGGCGGCAACCTTCTTAGAGAGACTGTGAGCACTGGAGAGCTGGCCAGAGAGGAAACCAACA	657
OY	595	AAGAAGGCGCTGTGAGGGGCTGTGGCCACTTTGTGTGAGATGGTCCCTCCCGGGGAAAC	654
Db	658	AAGAAGGCGCTGTGAGGGGCTGTGGCCACTTTGTGTGAGATGGTCCCTCCCGGGGAAAC	717
OY	655	CGCAACCCCTCTCAGCAAGGCGGTGGCCCAACAATGTGCAAGAGCAACACTGAGAGAG	714
Db	718	CGCAACCCCTCTCAGCAAGGCGGTGGCCCAACAATGTGCAAGAGCAACACTGAGAGAG	777
OY	715	AGGAGCTGTGCAAGTGAAGCTGTGCGCAAGGCTGAGGCGATGAGCTTTCYTGAGAGAGAC	774
Db	778	AGGAGCTGTGCAAGTGAAGCTGTGCGCAAGGCTGAGGCGATGAGCTTTCYTGAGAGAGAC	837
OY	775	CTTTTAAAGATTTGTGTGACAGGCTCTTCTAGACAAATTTCTGCAATGTGAAACTCTTGG	834
Db	838	CTTTTAAAGATTTGTGTGACAGGCTCTTCTAGACAAATTTCTGCAATGTGAAACTCTTGG	897
OY	835	AGATGGAACCAAGTGTCAAGCAAGTACTTCACTGAGTGTCAAGGTGCGGGGAAAGTGTGT	894
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 ORGANISM Homo sapiens

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 1 Xiao, Y.
 TITLE Regulation of human g protein-couple receptor kinase
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ACCESSION AF282269
VERSION AF282269.1 GI:17026317
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Osawa,S.
TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction
JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)
MEDLINE 21574315
PubMed 11717351
REFERENCE
AUTHORS Osawa,S. and Weiss,E.R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA
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Best Local Similarity 99.9%; Pred. No. 0;
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 AUTHORS Chen, C.K., Zhang, K., Church, K., Huang, W., Zhang, H.,
 Baehr, Y.J., Frederick, J.M., and Baehr, W.
 TITLE Characterization of human GRK7 as a potential cone opsin kinase
 JOURNAL Mol. Vis. 7, 305-313 (2001)
 MEDLINE 21626361
 PUBMED 11754336
 REFERENCE 2 (bases 1 to 1799)
 Baehr, W. and Chen, C.-K.
 DIRECT SUBMISSION Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15
 JOURNAL North/2030 East, Salt Lake City, UT 84112, USA
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DB 841 TGGCTCTCTTGAAGAAAGAAATCTTGGAGAGAGTCAAGAGCCCTTTCATTTGTCTCTG 900
QY 1054 CCTATGCTTTGAGAGAGAGAGCCATCTGCGCTTGTATGAGCTGATGAATGGGAGAG 1113
DB 901 CCTATGCTTTGAGAGAGAGAGCCATCTGCGCTTGTATGAGCTGATGAATGGGAGAG 960
QY 1114 ACCCTAGTTTCAACATCTAACAAGTGGGACAGCGTGGCTGAGATGAGCGGAGTACT 1173
DB 961 ACCCTAGTTTCAACATCTAACAAGTGGGACAGCGTGGCTGAGATGAGCGGAGTACT 1020
QY 1174 TTTTACTGGGCCAGATAGCTGTGGAGTGTGACCTCTCATGAATCTGGGATCTGTATC 1233
DB 1021 TTTTACTGGGCCAGATAGCTGTGGAGTGTGACCTCTCATGAATCTGGGATCTGTATC 1080
QY 1234 GGGACATGAAGCTGAGAGATGCTCTGATGATGACCTCGGACATGCAAGGTTATCTGAC 1293
DB 1081 GGGACATGAAGCTGAGAGATGCTCTGATGATGACCTCGGACATGCAAGGTTATCTGAC 1140
QY 1294 TGGGAGCTGGCCGTGAGATGAGAGGAGTGGCAAGCCATCAACAGAGGCTGGAAACAA 1353
DB 1141 TGGGAGCTGGCCGTGAGATGAGAGGAGTGGCAAGCCATCAACAGAGGCTGGAAACAA 1200
QY 1354 GTTATAGTGGCTCTGATGCTTATGAGAAAGGTAAGTTATCTTATCTGAGTCTGAT 1413
DB 1201 GTTATAGTGGCTCTGATGCTTATGAGAAAGGTAAGTTATCTTATCTGAGTCTGAT 1260
QY 1414 TTGCCATGAGATCAGACATTTATGAATGGTGTGAGAGACACATTCATGAAGTATCA 1473
DB 1261 TTGCCATGAGATCAGACATTTATGAATGGTGTGAGAGACACATTCATGAAGTATCA 1320
QY 1474 AGGAAAGGTCAATGAAGAGATCTGAAGCAAGAACTTGGCAAGAGAGTCAAAATTC 1533
DB 1321 AGGAAAGGTCAATGAAGAGATCTGAAGCAAGAACTTGGCAAGAGAGTCAAAATTC 1380
QY 1534 AGCATGATTAATTCAAGAGAGCAAGAAAGATTTTGAAGGCTCTTGGCTGAAGAAAC 1593
DB 1381 AGCATGATTAATTCAAGAGAGCAAGAAAGATTTTGAAGGCTCTTGGCTGAAGAAAC 1440
QY 1594 CAGAGCAACCTTAGAGAGCAGAGAAAGTGTGATGATCCAGAGAAACATCAATTTCTTA 1653
DB 1441 CAGAGCAACCTTAGAGAGCAGAGAAAGTGTGATGATCCAGAGAAACATCAATTTCTTA 1500
QY 1654 AAGCATCAACTTCTGCTGAGAGCTGAGCTTAATGAACCCCAATTTGTGCAAGC 1713
DB 1501 AAGCATCAACTTCTGCTGAGAGCTGAGCTTAATGAACCCCAATTTGTGCAAGC 1560
QY 1714 CTTGAGTGTATGCAAGAGCATGCTGAATTTGATGATTTCTGAGAGTTGGGAGG 1773
DB 1561 CTTGAGTGTATGCAAGAGCATGCTGAATTTGATGATTTCTGAGAGTTGGGAGG 1620
QY 1774 TGAATTTGATGCAAGAGTAAAGATTTCTTCAAAACCTTTCAGAGAGTGTCTTCTA 1833
DB 1621 TGAATTTGATGCAAGAGTAAAGATTTCTTCAAAACCTTTCAGAGAGTGTCTTCTA 1680
QY 1834 TGGCATGAGAGAGAAATTTATGAAGCGGAGCTTTGAGAGAACTGATGACCCCAACA 1893
DB 1681 TGGCATGAGAGAGAAATTTATGAAGCGGAGCTTTGAGAGAACTGATGACCCCAACA 1740
QY 1894 GACCTAGGAGGTTGAGAGAGGTAATTCATCAAGCTGGAGGAGTGTGTTGTTATTTGA 1952
DB 1741 GACCTAGGAGGTTGAGAGAGGTAATTCATCAAGCTGGAGGAGTGTGTTGTTATTTGA 1799

Db	481	TAGAGCATGGCTTTCTTTCGAAAGACAGCCCTTTAAGATTTTGATGACAGCGCTCTCA	540
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Db	541	CGACAAAGTTTCTGCACTGGAAAACCTTTCGAGATGCAACGATGTCAGACAAATGATCTTCAC	600
Qy	866	TGAGTTCAGAGATGCTGTGGGAAAAGGTGATTTTGGGAGGGTATGCGCGATCGAGTGGAAAAA	925
Db	601	TGAGTTCAGAGATGCTGTGGGAAAAGGTGATTTTGGGAGGGTATGCGCGATCGAGTGGAAAAA	660
Qy	926	CACGTGGGAAGATGATATGCTGTGAAGAACTGGAACAAGACGGCTGAGAAAAGAGGTGG	985
Db	661	CACGTGGGAAGATGATATGCTGTGAAGAACTGGAACAAGACGGCTGAGAAAAGAGGTGG	720
Qy	986	CGAGAAATGAGCTCTCTTGAAAAAGAAATCTTGGAGAGAGTCAAGACCTTTCAATGT	1045
Db	721	CGAGAAATGAGCTCTCTTGAAAAAGAAATCTTGGAGAGAGTCAAGACCTTTCAATGT	780
Qy	1046	CTCTCTGGGCTAATGCGCTTGAAGACAAACCAATCTGCGCTTGTCAAGACCGATGAA	1105
Db	781	CTCTCTGGGCTAATGCGCTTGAAGACAAACCAATCTGCGCTTGTCAAGACCGATGAA	840
Qy	1106	TGGGGGAGACCTCAAGGTTCACATCTCAACGTGGGACCGGTGGCTGGACAAGACCG	1165
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Qy	1166	GGTATCTTTTACTCGGACCAAGATAGCTGTGGAGTGTCTGACCTTCATGAATCGGCAAT	1225
Db	901	GGTATCTTTTACTCGGACCAAGATAGCTGTGGAGTGTCTGACCTTCATGAATCGGCAAT	960
Qy	1226	CGCTCTATCGGAGCATGAACCTGAGAGATGTGCTTCTGAGTGAACCTGGCACTGCAAGTT	1285
Db	961	CGCTCTATCGGAGCATGAACCTGAGAGATGTGCTTCTGAGTGAACCTGGCACTGCAAGTT	1020
Qy	1286	ATCTGACCTGGGGCTGGCCGTGAGATGAAAGGATGGCAAGCCATCAACCAAGGGCTGG	1345
Db	1021	ATCTGACCTGGGGCTGGCCGTGAGATGAAAGGATGGCAAGCCATCAACCAAGGGCTGG	1080
Qy	1346	AACCAATGGTTTACATGAGCTCTGAGATCTTAATGAAAAAGGTAAGTTTCTATCTGT	1405
Db	1081	AACCAATGGTTTACATGAGCTCTGAGATCTTAATGAAAAAGGTAAGTTTCTATCTGT	1140
Qy	1406	GGAATGTTTCCATGAGATGCAATTTTGAATGGTGTCTGGACAACAACATTTCAA	1465
Db	1141	GGAATGTTTCCATGAGATGCAATTTTGAATGGTGTCTGGACAACAACATTTCAA	1200
Qy	1466	AGATTACAAGAAAAGGTCAATGAAGAGATCTGAAGCAAAAACCTGCAAGACAGAGGT	1525
Db	1201	AGATTACAAGAAAAGGTCAATGAAGAGATCTGAAGCAAAAACCTGCAAGACAGAGGT	1260
Qy	1526	CAAAATCCAGCATGATATCTTCCAGAGAGCAAAAGATATTTGCAAGGCTCTTCTGGC	1585
Db	1261	CAAAATCCAGCATGATATCTTCCAGAGAGCAAAAGATATTTGCAAGGCTCTTCTGGC	1320
Qy	1586	TAAAGAACCAAGCAACGCTTAGAGACAGAGAAAAGCTGTAGATCCAGAGAAACATCA	1645
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Qy	1706	GGCAGACCTTCAAGTGGTTATGCCAAGACATGCGCTGAATTTGATGATTTCTCTGAGT	1765
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Db	1501	TCGGGGGGTGAATTTGATGACAAAGATTAAGCATTTCTTCAAAAACCTTTGGACAAGTGC	1560
Qy	1826	TGTTCCATATACATGCGACAGAAAGAAATTAATAGAAACGGGACTGTTTGAGAACTGAATGA	1885
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Qy	1886	CCCCAAGACCTTACGGGTGTGTGAGAGGGTATTCATCCAACTCTGGCGTGGTATTGTT	1945
	1621	CCCCAAGACCTTACGGGTGTGTGAGAGGGTATTCATCCAACTCTGGCGTGGTATTGTT	1680
Db	1946	ATTGTAAATTCCTCTCTTTACGACACGAGACAGAGATCTGGCGTGTGACATTAATCTTCCA	2005
Qy	1661	ATTGTAAATTCCTCTCTTTACGACACGAGACAGAGATCTGGCGTGTGACATTAATCTTCCA	1740
Db	2006	ATTGTTCACACGTGGAAATCT	2026
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RESULT	8
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LOCUS	AX797554 1659 bp DNA
DEFINITION	Sequence 3 from Patent WO02095032.
ACCESSION	AX797554
VERSION	AX797554.1 GI:37518056
KEYWORDS	
SOURCE	*
	Homo sapiens (human)
	linear PAT 04-OCT-2003

REFERENCE
1
Kapeller-Libermann, R. and Bandaru, R.
Method and compositions of human proteins and uses thereof.
Patent: WO 02095032-A 3 28-NOV-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
Location/Qualifiers

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Query Match	75.5%;	Score 1659;	DB 6;	Length 1659;
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QY	351	AAAGCCTCGACCTGGACAGCAGCAAAAGAGCTGACGCGCGGTAGCTGACCTGCCC	410
Db	61	AAAGCCTCGACCTGGACAGCAGCAAAAGAGCTGACGCGCGGTAGCTGACCTGCCC	120
QY	411	GGGCTGGAGGGCTGGCGGAGAGCTGCGCAGAAAGCTATCCCGAACTTCCAGAGCTGTGT	470
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Db	181	GAGCAGCAGCCATCGATGCGCTGGCGCTCTTCCGTGACTTCACGACCAAGTGCACAGTTC	240
QY	531	CGCAGGCGGCGACCTTCTTAGAGAGAGTGGCAAACTGGAGCTGGCGGAGAGAGACCC	590
Db	241	CGCAGGCGGCGACCTTCTTAGAGAGAGTGGCAAACTGGAGCTGGCGGAGAGAGACCC	300
QY	591	ACCAAGAAGCAGCGGCTGGAGGGGCTGTGGCCACTGTGGAGTGCCTGGCCCGGGGG	650
Db	301	ACCAAGAAGCAGCGGCTGGAGGGGCTGTGGCCACTGTGGAGTGCCTGGCCCGGGGG	360
QY	651	AAACCGCAACCTTCTCTAGCCAGCGAGCTGGGCCACCAAGTGGCAAGCAGACCACTGAG	710
Db	361	AAACCGCAACCTTCTCTAGCCAGCGAGCTGGGCCACCAAGTGGCAAGCAGACCACTGAG	420
QY	711	GAAAGCAGATGGCTGCAATGACGTGTGGCAAGGCTGAGGCACTGGCTTCTTGCAGAG	770
Db	421	GAAAGCAGATGGCTGCAATGACGTGTGGCAAGGCTGAGGCACTGGCTTCTTGCAGAG	480

[illegible]

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Qy 1911 GAGGGTAATTCATCCAACTGCGCGTGTGTATTG 1949

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AX642968 1662 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 45 from Patent WO01096547.
ACCESSION AX642968
VERSION AX642968.1 GI:28550117
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Yue, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A.R., Tribouley, C.M., Walla, N., Yao, M.G., Lu, D.A.,
Greenwald, S.R., Runkumar, J., Griffin, J.A., Kearney, L., Burford, N.,
Nguyen, D.B., Tang, T.T., Baughn, M.R., He, A., Thornton, M.,
Hafalla, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,
Recipon, S.A., Azimzal, Y., Policky, J.L., Ding, L., Grether, M.,
Elliot, V.S., Thangavelu, K., Batra, S. and Ison, C.H.
Humain kinases
Patent: WO 01096547-A 45 20-DEC-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1..1662
/mol_type="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 7477204CB1"

FEATURES
source

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Query Match 75.5%; Score 1658.8; DB 6; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 291 ATGATGACATGAGGAGGCTTGAACAACCTGATGCGCAACCGGCTTACCTGAGGCGG 350
Db 1 ATGATGACATGAGGAGGCTTGAACAACCTGATGCGCAACCGGCTTACCTGAGGCGG 60
Qy 351 AAGCCTTGGATGCGACAGCAAAAGAGCTGAGGCGGCGGCGTGAAGCTTGGCTTGGCC 410
Db 61 AAGCCTTGGATGCGACAGCAAAAGAGCTGAGGCGGCGGCGTGAAGCTTGGCTTGGCC 120
Qy 411 GGGCTGCAAGGAGGAGGAGCTGCGGCAAGAGCTGCTGTAACCTTCAACAGCTGTGT 470
Db 121 GGGCTGCAAGGAGGAGGAGCTGCGGCAAGAGCTGCTGTAACCTTCAACAGCTGTGT 180
Qy 471 GAGCAGCAAGCCTGATGCGCGCTTCTCGTGAATCTTCAAGCAAGTGGCCCAAGTTC 530
Db 181 GAGCAGCAAGCCTGATGCGCGCTTCTCGTGAATCTTCAAGCAAGTGGCCCAAGTTC 240
Qy 531 CGCAAGGCGGCAACCTTCTTAAGAGAGCTGAGAACTGGAGAGCTGGCCGAGAGGAGCC 590
Db 241 CGCAAGGCGGCAACCTTCTTAAGAGAGCTGAGAACTGGAGAGCTGGCCGAGAGGAGCC 300
Qy 591 ACCAAGAGCAGGAGGAGCTGAGAGGAGCTGAGAGCTTGTGCAAGTGGCCCTGAGGAG 650
Db 301 ACCAAGAGCAGGAGGAGCTGAGAGGAGCTGAGAGCTTGTGCAAGTGGCCCTGAGGAG 360
Qy 651 AACCCGCAACCTTCTTCAAGCAGGAGCTGAGCAACAGTGGCAAGCAAGCAAGCACTGAG 710
Db 361 AACCCGCAACCTTCTTCAAGCAGGAGCTGAGCAACAGTGGCAAGCAAGCAAGCACTGAG 420
Qy 711 GAGAGCAGTGGCTGAGAGAGCTGAGCGAGAGCTGAGAGCTTGTGCAAGTGGCTTGTGCAAG 770
Db 421 GAGAGCAGTGGCTGAGAGAGCTGAGCGAGAGCTGAGAGCTTGTGCAAGTGGCTTGTGCAAG 480

Qy 771 CAGCCCTTTAAGATTTGTGACCAAGGCTTTTACCAAGATTTTGTGCAAGTGGAAATC 830
Db 481 CAGCCCTTTAAGATTTGTGACCAAGGCTTTTACCAAGATTTTGTGCAAGTGGAAATC 540
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Db 541 TTGAGATGCAACAGAGTGTGAGCAAGATCTTCACTAGTTCAAGATGCTGGGAGAGGT 600
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Qy 1011 GAAATCTTGGAGAGAGTGTGAGAGGCTTCACTTGTCTGTGAGCTTGTGAGAGG 1070
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Qy 1071 AAGACCATCTGAGCTTGTGATGAGCTGATGAGTGGGAGGAGGAGGAGGAGGAGGAG 1130
Db 781 AAGACCATCTGAGCTTGTGATGAGCTGATGAGTGGGAGGAGGAGGAGGAGGAGGAG 840
Qy 1131 TACACGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
Db 841 TACACGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 1191 GCTGTGGAGATGTGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGAT 1250
Db 901 GCTGTGGAGATGTGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGAT 960
Qy 1251 AATGTGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGAT 1310
Db 961 AATGTGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTTGTGAT 1020
Qy 1311 ATGAGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1370
Db 1021 ATGAGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1371 ATCTTAATGGAAGAGTGAATTTCTTCTTGTGAGCTTGTGAGCTTGTGAGCTTGTGAG 1430
Db 1081 ATCTTAATGGAAGAGTGAATTTCTTCTTGTGAGCTTGTGAGCTTGTGAGCTTGTGAG 1140
Qy 1431 ATTTATGAATGGTGTGAGCAAGCAATCAAGATTAAGAGGAGGAGGAGGAGGAGGAG 1490
Db 1141 ATTTATGAATGGTGTGAGCAAGCAATCAAGATTAAGAGGAGGAGGAGGAGGAGGAG 1200
Qy 1491 GAGGATCTGAAGCAAGCAATCTGCAAGAGAGGATCAATCTGAGATGATTAATCTTACA 1550
Db 1201 GAGGATCTGAAGCAAGCAATCTGCAAGAGAGGATCAATCTGAGATGATTAATCTTACA 1260
Qy 1551 GAGGAGCAAGAGATTTTGAAGGCTTCTTGTGAGCTTGTGAGCTTGTGAGCTTGTGAG 1610
Db 1261 GAGGAGCAAGAGATTTTGAAGGCTTCTTGTGAGCTTGTGAGCTTGTGAGCTTGTGAG 1320
Qy 1611 AGCAGAGAGAGATCTGATGATCCAGAGAACTATTTCTTAAACAGTCAACTTCTTCT 1670
Db 1321 AGCAGAGAGAGATCTGATGATCCAGAGAACTATTTCTTAAACAGTCAACTTCTTCT 1380
Qy 1671 CGCCTGAGAGCTGAGCTTATGAAACCCCAATTTGTGCAAGCTTCAAGTGTATATGCC 1730
Db 1381 CGCCTGAGAGCTGAGCTTATGAAACCCCAATTTGTGCAAGCTTCAAGTGTATATGCC 1440
Qy 1731 AAAGCATCGCTGAATTTGATGATTTCTTGAAGTTGGGAGGAGGAGGAGGAGGAGGAG 1790
Db 1441 AAAGCATCGCTGAATTTGATGATTTCTTGAAGTTGGGAGGAGGAGGAGGAGGAGGAG 1500
Qy 1791 GATAGAGAGTCTTCAAAACCTTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1850
Db 1501 GATAGAGAGTCTTCAAAACCTTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560

QY	1851	ATTATATGAAACGGGACCTGTTTATGAGCACTGTAATGACCCCAAGACCTTCGGCTTGGAG	1910
Db	1561	ATTATGAAACGGGACCTGTTTATGAGCACTGTAATGACCCCAAGACCTTCGGCTTGGAG	1620
QY	1911	GAGGCTAATTATCCAAAGTCGTGGCGTGTGTTTATTGTGTA	1952
Db	1621	GAGGCTAATTATCCAAAGTCGTGGCGTGTGTTTATTGTGTA	1662

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LOCUS	AR225817	1662 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 1 from patent US 6444456.				
ACCESSION	AR225817				
VERSION	AR225817.1	GI:27263947			

Query Match	75.5%	Score 1658.4;	DB 6;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1659; Conservative	1;	Mismatches	2;	Indels 0; Gaps 0;

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QY	351	AAGCCCTCGGACTGCGACAGCAAAAGAGCTGAGCGGCGCGCTGATGCTGAGCCCTTGCC	410
Db	61	AAGCCCTCGGACTGCGACAGCAAAAGAGCTGAGCGGCGCGCTGATGCTGAGCCCTTGCC	120
QY	411	GGGCTCGAGGGCTGCGCGAGCTCCGCGAAGAGCTGTCCCTGAACTTCCACAGCCTGTGT	470
Db	121	GGGCTCGAGGGCTGCGCGAGCTCCGCGAAGAGCTGTCCCTGAACTTCCACAGCCTGTGT	180
QY	471	GAGCGACAGCCCATATGGATGCGCGCCCTCTTCCTGATCTTCTTAAGCAAGTGGCCACGTTC	530
Db	181	GAGCGACAGCCCATATGGATGCGCGCCCTCTTCCTGATCTTCTTAAGCAAGTGGCCACGTTC	240
QY	531	CGCAGAGCGGCAACCTTCTTAAGAGGACGTGCACAACTGAGGAGCTGGCCAGAGAGGAGACC	590
Db	241	CGCAGAGCGGCAACCTTCTTAAGAGGACGTGCACAACTGAGGAGCTGGCCAGAGAGGAGACC	300
QY	591	ACCAAAAGACAGCGCGCTGAGAGGAGCTGTGTGCACTTGTGAGATGCCCCCTGCGGAG	650
Db	301	ACCAAAAGACAGCGCGCTGAGAGGAGCTGTGTGCACTTGTGAGATGCCCCCTGCGGAG	360
QY	651	AACCGCAACCCCTTCTTCAGCCAGAGCGGTGGCCACAAGTGCACAAAGTGCACACACTGAG	710
Db	361	AACCGCAACCCCTTCTTCAGCCAGAGCGGTGGCCACAAGTGCACAAAGTGCACACACTGAG	420
QY	711	GAAAGACAGATGAGCTGAGTGAAGCTGTGCGCAAGGCTGAGAGCCATGAGCTTTCTTGCAAG	770
Db	421	GAAAGACAGATGAGCTGAGTGAAGCTGTGCGCAAGGCTGAGAGCCATGAGCTTTCTTGCAAG	480
QY	771	CAGCCCTTTAAGATTTTCGTGACAGAGCCCTTCTTACGACAAGTTTCTGAGTGGAAATC	830
Db	481	CAGCCCTTTAAGATTTTCGTGACAGAGCCCTTCTTACGACAAGTTTCTGAGTGGAAATC	540
QY	831	TTTGAGATGCAACAAGATGTCACAGCAAGTACTTCACTGATCTCAGATGCTGGGGGAAAAGT	890
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Db	601	GGTTTGGGAGGTAATGCGCTCCAGGTGAAAACACTGGGAGAAATGTAATGCTGTAG	660
Qy	951	AAACTGAGCAGAAAGCGGCTGAAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG	1010
Db	661	AAACTGAGCAGAAAGCGGCTGAAAGAAAGAGTGGCGAGAGATGGCTCTCTTGGAAAG	720
Qy	1011	GAATCTTGGAGAGGTCAAGAGCCCTTATATGTCTCTGGCTATATGCTTGGAGC	1070
Db	721	GAATCTTGGAGAGGTCAAGAGCCCTTATATGTCTCTGGCTATATGCTTGGAGC	780
Qy	1071	AAGCCATCTCTGCTCTGATGAGCCTGATTAATGGGGGAGACCTCAAGTGCATC	1130
Db	781	AAGCCATCTCTGCTCTGATGAGCCTGATTAATGGGGGAGACCTCAAGTGCATC	840
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Qy	1191	GCGTGGGAGATGCTGCACCTCCATGAATCTGGGATCGTATGGGACATGAACCTGAG	1250
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Qy	1251	AATGCTCTTGATGATCACTCGGCACTGCAAGGTATATGACTCGGGCTGGCGTGAG	1310
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Qy	1371	ATCCTAATGAAAAAGGTAAATTCTTACTCTGGAGACTGGTTTGCATGGAGTCAAC	1430
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Qy	1491	GAGGATCTGAAAGCAAAAGAACTCTGCAAGCGAGGTCAATTCAGATGATAACTACA	1550
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Qy	1551	GAGAGCAAAAGATATTGGCAGGCTCTTCTGGCTAAGAAACAGAGCAACGTTAGGA	1610
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Qy	1611	AGCAGAGAAAGTCTGATGATCCAGGAAACATCTTCTTTAAACATCACTTCT	1670
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Qy	1851	ATTATGAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAAGACCTAAGGGTTGTAG	1910
Db	1561	ATTATGAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAAGACCTAAGGGTTGTAG	1620
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Db	1621	GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTTGAA	1662

RESULT 11
 AX252439 1662 bp DNA linear PAT 05-OCT-2001
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 DEFINITION Sequence 1 from Patent WO0168869.
 ACCESSION AX252439
 VERSION AX252439.1 GI:15985733
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Walke, D.W., Miljanowski, N.L. and Turner, C.A.
 Human g-coupled protein receptor kinases and polymucleotides
 encoding the same
 Patent: WO 0168869-A 1 20-SEP-2001;
 JOURNAL Lexicon Genetics Incorporated (US)
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 Query Match 75.5%; Score 1658.4; DB 6; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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 LOCUS
 DEFINITION Sequence 1 from patent US 6331423.

ACCESSION AR263766
 VERSION AR263766.1 GI:28075747
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unpublished.
 1 (bases 1 to 1662)
 AUTHORS Giegler, K., Beasley, E.M. and Di Francesco, V.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
 JOURNAL Patent: US 631423-A 18-DEC-2001;
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ORIGIN

Query Match 75.4%; Score 1657.2; DB 6; Length 1662;
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 Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 VERSION AR343544.1 GI:3739257
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unpublished.
 1 (bases 1 to 1662)
 AUTHORS Giegler, K., Beasley, E.M. and Di Francesco, V.

TITLE Isolated human kinase proteins, nucleic acid molecules encoding

human kinase proteins, and uses thereof

Patent: US 6579709-A 1 17-JUN-2003;

FEATURES Location/Qualifiers

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ORIGIN

Query Match 75.4%; Score 1657.2; DB 6; Length 1662;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 LOCUS AX357902
 DEFINITION Sequence 1 from Patent WO0192496.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Guejler, K., di Francesco, V., and Beasley, E. M.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding
 human kinase proteins, and uses thereof
 JOURNAL Patent: WO 0192496-A 1 06-DEC-2001;
 Apptera Corporation Robert A. Millman Assistant Secretary (US)
 FEATURES Location/Qualifiers
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Query Match 75.4%; Score 1657.2; DB 6; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGGTGGACATGGGGGCTCTGAGCAACCTGATCCGCAACCGGCTACCTGACAGGCGCG 350
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LOCUS AX166511
DEFINITION Sequence 2 from Patent WO0138503.
ACCESSION AX166511
VERSION AX166511.1 GI:14546856
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Plozman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
Flanagan, P., and Clary, D.S.

TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 2 31-May-2001;

FEATURES
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source

ORIGIN /organism="Homo sapiens"
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Db 481 CAGCCCTTAAAGATTTCGTGACAGCGCTTCTACGACAACTTCTGCACTGCAATC 540
QY 831 TTCGAGATGCAACAGTGCAGACAACTTCTGAGTTCAGAGTTCGAGGAGGAGAAAGT 890
Db 541 TTCGAGATGCAACAGTGCAGACAACTTCTGAGTTCAGAGTTCGAGGAGGAGAAAGT 600
QY 891 GGTTCGAGGAGTATGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 950
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QY 951 AAACCTGACAAAGAGCGCTGAAAGAAAGAGTGGCGAGAGATGCTCTTGGAAAAG 1010
Db 661 AAACCTGACAAAGAGCGCTGAAAGAAAGAGTGGCGAGAGATGCTCTTGGAAAAG 720
QY 1011 GAAATCTTGGAGAAAGGTCAGCAGCCCTTCTCATGTCCTCTGCGCTATGCTTGAAGC 1070
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QY 1191 GCTGTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
Db 901 GCTGTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1251 AATGTGCTTCTGAGTGAATCTGAGCACTGAGGTTATCTGACTGAGGCTGAGCTGAG 1310
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Db 1321 AGCAGGAAAAGTCTGATGATCCAGGAAACATCATTTCTTAAAGGATCACTTCT 1380
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Job time : 5731.66 secs

Sheet 1

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 14:01:20 ; Search time 523.034 Seconds

(without alignments)
15563.146 Million cell updates/sec

Title: US-10-044-205a-3

Perfect score: 1659
Sequence: 1 atggtgagacatgggggccccct.....ctggcggtgtgtttatctg 1659

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/prodata/2/pubna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/2/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/2/pubna/US06_PUBCOMB.seq.*
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- 18: /cgn2_6/prodata/2/pubna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/prodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1659	100.0	1659	14	US-10-044-205a-3
2	1659	100.0	2198	14	US-10-044-205a-1
3	1655.8	99.8	1662	17	US-10-311-034-45
4	1655.8	99.8	1662	17	US-10-451-168-49
5	1655.8	99.8	2249	15	US-10-217-745-5
6	1654.2	99.7	1662	15	US-10-217-745-1
7	1654.2	99.7	1662	9	US-09-964-469-1
8	1589.8	95.8	1701	13	US-10-425-963-1
9	1589.8	95.8	1701	13	US-10-072-012-273
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11	1617.4	37.2	36651	15	US-09-964-469-3
12	1617.4	37.2	36651	15	US-10-425-963-3
13	418.2	25.2	2848	10	US-09-851-686-2
14	418.2	25.2	2848	10	US-09-873-367C-142

15	418.2	25.2	2848	16	US-10-159-856-4	Sequence 4, Appl 1
16	400.6	24.1	2817	16	US-10-388-934-621	Sequence 621, App
17	379.4	22.9	2467	15	US-10-084-817-110	Sequence 110, App
18	377.8	22.8	2519	14	US-10-071-766-13	Sequence 13, Appl
19	374.6	22.6	2519	10	US-09-971-392-72	Sequence 72, Appl
20	373	22.5	2511	15	US-10-072-036-60	Sequence 60, Appl
21	373	22.5	2529	15	US-10-072-036-42	Sequence 42, Appl
22	373	22.5	2557	9	US-09-972-694-1	Sequence 4, Appl
23	373	22.5	2557	12	US-10-380-235-7	Sequence 7, Appl 1
24	373	22.5	2557	12	US-10-305-720-1298	Sequence 1298, Ap
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26	320.6	19.3	1737	15	US-10-325-430-2	Sequence 2, Appl 1
27	320.6	19.3	2113	15	US-10-325-430-1	Sequence 1, Appl 1
28	158.4	9.5	493	10	US-09-918-995-17835	Sequence 1, Appl 1
29	153.4	9.2	3154	10	US-09-955-999-45	Sequence 37835, A
30	151	9.1	1679	9	US-09-771-161A-25	Sequence 45, Appl
31	151	9.1	2037	13	US-10-087-664-23	Sequence 25, Appl
32	151	9.1	2037	13	US-10-218-779-23	Sequence 23, Appl
33	151	9.1	2070	15	US-10-038-010-47	Sequence 47, Appl
34	151	9.1	3073	13	US-10-029-020-11	Sequence 11, Appl
35	151	9.1	3268	15	US-10-247-671-3	Sequence 47, Appl
36	144.6	8.7	1377	16	US-10-264-049-482	Sequence 1306, Ap
37	132.8	8.0	2909	12	US-10-152-319A-1465	Sequence 1465, Ap
38	132.4	8.0	2683	16	US-10-152-319A-1539	Sequence 1539, Ap
39	132.4	8.0	2683	16	US-10-191-803-38	Sequence 38, Appl
40	130.8	7.9	2067	16	US-10-305-720-1306	Sequence 1306, Ap
41	129.2	7.8	1411	10	US-09-955-999-14	Sequence 14, Appl
42	129.2	7.8	2067	15	US-10-038-010-49	Sequence 49, Appl
43	127.6	7.7	2362	15	US-10-037-270-273	Sequence 273, App
44	127.6	7.7	2362	16	US-10-117-722-273	Sequence 273, App
45	112.4	6.8	1661	13	US-10-087-192-989	Sequence 989, App

ALIGNMENTS

RESULT 1
US-10-044-205a-3
Sequence 3, Appl 1
Publication No. US02002123464A1
GENERAL INFORMATION:
APPLICANT: KAPTELIER, LIBERMANN, Rosana
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
FILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044, 205A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242, 428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/241, 884
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241, 877
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1659
TYPE: DNA
ORGANISM: Homo sapiens
US-10-044-205a-3

Query Match 100.0%; Score 1659; DB 14; Length 1659;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGACATGGGAGCCCTGACACCTGATCGCCAAACGCGCTTACGAGCCCGG 60
DB 1 ATGCTGACATGGGAGCCCTGACACCTGATCGCCAAACGCGCTTACGAGCCCGG 60
QY 61 AAGCCTGAGACTCGACACGACAAAGCTGAGAGGCGGCGCGCTGAGCTGCGCCCTG 120
DB 61 AAGCCTGAGACTCGACACGACAAAGCTGAGAGGCGGCGCGCTGAGCTGCGCCCTG 120

QY 121 GGGCTGACGAGGCTGCGGAGGCTCGGACAGAGCTGTCTTAACTTCCACAGCTGTGT 180
 DB 121 GGGCTGACGAGGCTGCGGAGGCTCGGACAGAGCTGTCTTAACTTCCACAGCTGTGT 180
 QY 181 GAGCAGACCCCATCGGTGGCGGCTCTTCCGTGACCTTCAAGCCACAGGCTTC 240
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 DB 421 GAAGACAGAGCTGCAAGGAGCTGTGCAAGGAGCTGTGCAAGGAGCTTGGCGAGGAGCC 480
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 QY 541 TTGAGAGAGCAAGGAGCTGTGCAAGGAGCTGTGCAAGGAGCTTGGCGAGGAGCC 600
 DB 541 TTGAGAGAGCAAGGAGCTGTGCAAGGAGCTGTGCAAGGAGCTTGGCGAGGAGCC 600
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 DB 601 GCTTTTGGGAGGATGTGCGCTCCAGGTGAAAAAAGCTGGAGAGATGTATGCTGTAAAG 660
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 QY 781 AAGACCATCTCTGCTTGTATGAGCTGTGCAAGGAGCTTGGCGAGGAGCC 840
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 DB 841 TACAGAGTGGGAGAGGCTGTGCAAGGAGCTGTGCAAGGAGCTTGGCGAGGAGCC 900
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 QY 1561 ATTATAG 1620
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RESULT 2
 US-10-044-205A-1
 ; Sequence 1, Application US/10044205A
 ; Publication No. US20020123464A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KAPILLER-LIBERMAN, Rosana
 ; APPLICANT: BANDARU, Rajasekhari
 ; TITLE OF INVENTION: Uses thereof
 ; FILE REFERENCE: 10147-52U1
 ; CURRENT APPLICATION NUMBER: US/10/044, 205A
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/242,428
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: US 60/241,884
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: US 60/241,877
 ; PRIOR FILING DATE: 2000-10-20
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2198
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-044-205A-1

Query Match 100.0%; Score 1659; DB 14; Length 2198;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTGAAG 60
 DB 291 ATGAGTGAAG 350
 QY 61 AAGCCCTGAG 120
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 QY 121 GGGCTGACGAGGCTGCGGAGGCTCGGACAGAGCTGTCTTAACTTCCACAGCTGTGT 180

Db 411 GAGCTGACAGGAGCTGCGGAGCTCCGACAGAGCTGTCCTGAACTTCCAGAGCTGTGT 470
Qy 181 GAGAGAGAGCCATGAGTGTGCGGCTCTTCCGTGACTTCTGACCAAGCTGCCAGCTTTC 240
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Db 591 ACCAAGAGAGCGGCTGACAGAGGCTGTGTGAGCACTTGTGAGTGTGCCCTGCGCGAGG 650
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Qy 721 GAAATCTTGAAGAGAGTCAAG 780
Db 1011 GAAATCTTGAAGAGAGTCAAG 1070
Qy 781 AAGACCCATCTGCTGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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Db 1251 AATGTCCTTCTGATGAG 1310
Qy 1021 ATGAAGGTTGAG 1080
Db 1311 ATGAAGGTTGAG 1370
Qy 1081 ATCTTAATGAG 1140
Db 1371 ATCTTAATGAG 1430
Qy 1141 ATTATGAAGTGTGAG 1200
Db 1431 ATTATGAAGTGTGAG 1490
Qy 1201 GAGAGTCTGAAG 1260
Db 1491 GAGAGTCTGAAG 1550

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Db 1731 AAG 1790
Qy 1501 GATAG 1560
Db 1791 GATAG 1850
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Db 1851 ATTATGAAG 1910
Qy 1621 GAGGATATTCATCCAG 1680
Db 1911 GAGGATATTCATCCAG 1940

RESULT 3
US-10-311-034-45
Sequence 45, Application US/10311034
Publication No. US20040023242A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BOROMSKY, Mark L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Yan
APPLICANT: GANDHI, Ameena R.
APPLICANT: TRIBOLEY, Catherine M.
APPLICANT: CHAMLA, Narinder K.
APPLICANT: YAO, Monique G.
APPLICANT: LU, Dyrng Aina M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: RANKOWAR, Jayalaxmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Daniel B.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAWALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURUBALAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KHAN, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Valde
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT

Query Match	99.8%	Score 1655.8	DB 17	Length 1662
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1657; Conservative	0	Mismatches 2	Indels 0	Gaps 0

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Db	781	AAAGACCCATCTTCGCGCTTCATGAGACCCGAGTGAATGAGGAGAGACCTCAAGTTCCACATC	840
QY	841	TAACAACGTGGGACACGCGTGGCTGGACATGAGCCGGGTGATCTTTATCTCGGCCAGATA	900
Db	841	TAACAACGTGGGACACGCGTGGCTGGACATGAGCCGGGTGATCTTTATCTCGGCCAGATA	900
QY	901	GCCTGTGGGATGCTTGACCTTCATGAATCTGGCATCTGTCTATCTGGGACATGAGCCTGAG	960
Db	901	GCCTGTGGGATGCTTGACCTTCATGAATCTGGCATCTGTCTATCTGGGACATGAGCCTGAG	960
QY	961	AATGTGCTTCTGGATGACCTCGGCGAATCGAGAGTTATCTGACCTCGGGCTGGCCGTGAG	1020
Db	961	AATGTGCTTCTGGATGACCTCGGCGAATCGAGAGTTATCTGACCTCGGGCTGGCCGTGAG	1020
QY	1021	ATGGAAGGGTGGCAAGCCCATCACAGAGGGGTGGAAACAAATGTTATACATGCTCTGAG	1080
Db	1021	ATGGAAGGGTGGCAAGCCCATCACAGAGGGGTGGAAACAAATGTTATACATGCTCTGAG	1080
QY	1081	ATCCTATATGAAAAAGGTAAATTATCTATCTGTGGAATGTTGGTCCATGGGATCGAGC	1140
Db	1081	ATCCTATATGAAAAAGGTAAATTATCTATCTGTGGAATGTTGGTCCATGGGATCGAGC	1140
QY	1141	ATTATTGAAATGCTGTCTGGAGCAACCACTCAAAAGATTACAAGSAAAAGTCAAGTAA	1200
Db	1141	ATTATTGAAATGCTGTCTGGAGCAACCACTCAAAAGATTACAAGSAAAAGTCAAGTAA	1200
QY	1201	GAGGATCTGGAAGCAAGAACTCTCTGACAGACGAGTCAATTCGAGATGATTAATCTTACA	1260
Db	1201	GAGGATCTGGAAGCAAGAACTCTCTGACAGACGAGTCAATTCGAGATGATTAATCTTACA	1260
QY	1261	GAGGAGCAAAAGATATTGAGGCTCTTCTGGCTTAAGAAACAGAGCAACGCTTAGGA	1320
Db	1261	GAGGAGCAAAAGATATTGAGGCTCTTCTGGCTTAAGAAACAGAGCAACGCTTAGGA	1320
QY	1321	AGCAGAGAAAAGTCTGATGATCTCCAGAGAAACATATTTCTTTAAACATCAATCTTCT	1380
Db	1321	AGCAGAGAAAAGTCTGATGATCTCCAGAGAAACATATTTCTTTAAACATCAATCTTCT	1380
QY	1381	CGCCTGGAAGCTGGCCATATGAAACCCCATTTGTGCGAGCCCTTCAGTGGTTATGCG	1440
Db	1381	CGCCTGGAAGCTGGCCATATGAAACCCCATTTGTGCGAGCCCTTCAGTGGTTATGCG	1440
QY	1441	AAAGACATCGCTGAATATGATTTCTCTGAGGTTCCGGGGGTGGAAATTGATGACAA	1500
Db	1441	AAAGACATCGCTGAATATGATTTCTCTGAGGTTCCGGGGGTGGAAATTGATGACAA	1500
QY	1501	GATPAACAGTTCTTCAAAAACCTTGGCAGACGGTGTCTTATGACATGCGAGAGAA	1560
Db	1501	GATPAACAGTTCTTCAAAAACCTTGGCAGACGGTGTCTTATGACATGCGAGAGAA	1560
QY	1561	ATTATGAAACGGGACATGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGAG	1620
Db	1561	ATTATGAAACGGGACATGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGAG	1620
QY	1621	GAGGTTATTCATCCAGTCTGGCGTGTGTTGTTATTG	1659
Db	1621	GAGGTTATTCATCCAGTCTGGCGTGTGTTATTG	1659
RESULT 4			
US-10-451-168-49			
/ Sequence 49, Application US/10451168			
/ Publication No. US20040091969A1			
/ GENERAL INFORMATION:			
/ APPLICANT: SMITHKLINE BEECHAM CORPORATION			
/ APPLICANT: SMITHKLINE BEECHAM P.L.C.			
/ APPLICANT: GLAXO GROUP LIMITED			
/ TITLE OF INVENTION: NOVEL COMPOUNDS			
/ FILE REFERENCE: GP50039			
/ CURRENT APPLICATION NUMBER: US/10/451,168			
/ CURRENT FILING DATE: 2003-11-12			

QY 1 ATGTGGACATGAGGGGGCCCTGGACAACTGATGCGCCAAACCGCTCTACTGAGAGCCGG 60

Db 1 ATGTGGACATGAGGGGGCCCTGGACAACTGATGCGCCAAACCGCTCTACTGAGAGCCGG 60

QY 61 AAGCCTCTGGACTGGACAGCAAGAAGCTGAGAGCGCGCGCGCTGAGCTGAGCCCTTGGCC 120

Db 61 AAGCCTCTGGACTGGACAGCAAGAAGCTGAGAGCGCGCGCGCTGAGCTGAGCCCTTGGCC 120

QY 121 GGGCTGGAGGGCTGGGGGAGCTCGGCCAAGAGCTGTCTCTGAACTTTCACAGCTGTGT 180

Db 121 GGGCTGGAGGGCTGGGGGAGCTCGGCCAAGAGCTGTCTCTGAACTTTCACAGCTGTGT 180

QY 181 GAGCAGCAGCCCATGCTCGCGCCCTTCCGATGACTTCTGATGCAACTGCGCCAGCTTC 240

Db 181 GAGCAGCAGCCCATGCTCGCGCCCTTCCGATGACTTCTGATGCAACTGCGCCAGCTTC 240

QY 241 CGCAGACGCGCACTTCTCTAAGAGACGTGCAGAACTGAGACTGCGCGAGAGAGACC 300

Db 241 CGCAGACGCGCACTTCTCTAAGAGAGCTGCAGAACTGAGAGCTGCGCGAGAGAGACC 300

QY 301 ACCAAGACAGAGGCGCTGACAGGGGGCTGTGGCCACTGTGTGAGTGCCTTGGCCCGGG 360

Db 301 ACCAAGACAGAGGCGCTGACAGGGGGCTGTGGCCACTGTGTGAGTGCCTTGGCCCGGG 360

QY 361 AACCCGCAACCTTCTCTACAGCAGCGCGTGGCCCACTAAGTGCAGACAGCCACCATGAG 420

Db 361 AACCCGCAACCTTCTCTACAGCAGCGCGTGGCCCACTAAGTGCAGACAGCCACCATGAG 420

QY 421 GAAGACGAGGTGCTGATGAGACGCTGCGAAGGCTGAGGCTAGGCTTCTTGGCAAG 480

Db 421 GAAGACGAGGTGCTGATGAGACGCTGCGAAGGCTGAGGCTAGGCTTCTTGGCAAG 480

QY 481 CAGCCCTTTAAGATTTCGTGACAGAGCCCTTCTACAGCAAGTTCTCTGAGTGGAAATC 540

Db 481 CAGCCCTTTAAGATTTCGTGACAGAGCCCTTCTACAGCAAGTTCTCTGAGTGGAAATC 540

QY 541 TTGGAATGCAACAGGTGCAGACAACTACTGATTCCTGAGTCTGGGAAAAGT 600

Db 541 TTGGAATGCAACAGGTGCAGACAACTACTGATTCCTGAGTCTGGGAAAAGT 600

QY 601 GGTTTTGGAGGATATGTCGCTCAGGTGAAAAAACACTGGGAAGATGATGCTGTAG 660

Db 601 GGTTTTGGAGGATATGTCGCTCAGGTGAAAAAACACTGGGAAGATGATGCTGTAG 660

QY	661	AAACGTGCAAGAAAGGCGCTAAGAAAGAAAGTGGCCAGAAATGGCTCTCTGGAAAG	720
Db	661	AAACTGCAAGAAAGGCGCTAAGAAAGAAAGTGGCCAGAAATGGCTCTCTGGAAAG	720
QY	721	GAATCTTGGAGAGAGTCAAGAGCCCTTTCATGTCTCTCGGCGCTAATCCCTTGAAGC	780
Db	721	GAATCTTGGAGAGAGTCAAGAGCCCTTTCATGTCTCTCGGCGCTAATCCCTTGAAGC	780
QY	781	AAGACCCATCTCGCTTGTGTCATGAAGCTGTAGATGGGGGAGACCTCAAGTCCACATC	840
Db	781	AAGACCCATCTCGCTTGTGTCATGAAGCTGTAGATGGGGGAGACCTCAAGTCCACATC	840
QY	841	TAGACGTGTGGACCCCGTGGCTTGAACATGAACCGGGGTATCTTTTATCTCGGCCAGATA	900
Db	841	TAGACGTGTGGACCCCGTGGCTTGAACATGAACCGGGGTATCTTTTATCTCGGCCAGATA	900
QY	901	GCCGTGGGATCTGCACTTCATGAACTCCGACATCGTATGGGACATGAACCTGGAG	960
Db	901	GCCGTGGGATCTGCACTTCATGAACTCCGACATCGTATGGGACATGAACCTGGAG	960
QY	961	AAATGCTTCTGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCGTGGCGTGGAG	1020
Db	961	AAATGCTTCTGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGCGTGGCGTGGAG	1020
QY	1021	ATGAAGGGTGGCAAGCCCATCAACCGAGGGCGTGGAAACCAATGTTATATGGCTCTGAG	1080
Db	1021	ATGAAGGGTGGCAAGCCCATCAACCGAGGGCGTGGAAACCAATGTTATATGGCTCTGAG	1080
QY	1081	ATCTATATGAAAAGGTATGTTATTCATCTGATCTGTGACCTGGTTGCCATGGGATCGAC	1140
Db	1081	ATCTATATGAAAAGGTATGTTATTCATCTGATCTGTGACCTGGTTGCCATGGGATCGAC	1140
QY	1141	ATTATGAAATGTGTGCTGGAAGAACCCATTCAAAGATTACAGAAAAGCTCAGTAA	1200
Db	1141	ATTATGAAATGTGTGCTGGAAGAACCCATTCAAAGATTACAGAAAAGCTCAGTAA	1200
QY	1201	GAGGATCTGAAGCAAAAGAACTCTGGAAACGAGGTCAATTCAGACATGATATCTTACA	1260
Db	1201	GAGGATCTGAAGCAAAAGAACTCTGGAAACGAGGTCAATTCAGACATGATATCTTACA	1260
QY	1261	GAGGAGCAAAAAGTATTTGCAAGGCTCTTCTGGCTTAAAGAACAGAGCAAGCTTAGGA	1320
Db	1261	GAGGAGCAAAAAGTATTTGCAAGGCTCTTCTGGCTTAAAGAACAGAGCAAGCTTAGGA	1320
QY	1321	AGCAGAGAAAAGTCTGATGATCCCAAGAAAACATCATTTCTTTAAACGATCACTTCTCT	1380
Db	1321	AGCAGAGAAAAGTCTGATGATCCCAAGAAAACATCATTTCTTTAAACGATCACTTCTCT	1380
QY	1381	CGCCTGGAAGCTGGCTTAATTTGAACCCCAATTTGTGCAAGCCCTTGAGGTATTATGCC	1440
Db	1381	CGCCTGGAAGCTGGCTTAATTTGAACCCCAATTTGTGCAAGCCCTTGAGGTATTATGCC	1440
QY	1441	AAAGCATCGTGAATTTGATGATTTCTCGAGGTCGAGGGGTGGAATTTGATGACAA	1500
Db	1441	AAAGCATCGTGAATTTGATGATTTCTCGAGGTCGAGGGGTGGAATTTGATGACAA	1500
QY	1501	GATTAAGAGTTCTTAAAAACCTTTGGACAGAGTGTCTTTCTATAGATGTGCGAGAGAA	1560
Db	1501	GATTAAGAGTTCTTAAAAACCTTTGGACAGAGTGTCTTTCTATAGATGTGCGAGAGAA	1560
QY	1561	ATTATGAAAAAGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTGTGAG	1620
Db	1561	ATTATGAAAAAGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTGTGAG	1620
QY	1621	GAGGGTAAATCAATCCAAATCTGAGGTGTGTGTTTATTG	1659
Db	1621	GAGGGTAAATCAATCCAAATCTGAGGTGTGTGTTTATTG	1659

RESULT 5
US-10-217-745-5
: Sequence 5, Application US/10217745

Query Match	99.8%	Score 1655.8;	DB 15;	Length 2249;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0.

QY	721	GAATCTTGAGAGGTGAGACCCCTTTCA	TGTCTCTCTGAGCTTAAGCTTTAGAGC	780
Db	1074	GAATCTTGAGAGAGTACAGACCCCTTTCAT	TTCTCTCTGAGCTTAAGCTTTAGAGC	1133
QY	781	AAGACCCATCTGCTGCTTCATGAGCCGTAT	TGAATGGAGGAGAACCTCAATTCACATC	840
Db	1134	AAGACCCATCTGCTGCTTCATGAGCCGTAT	TGAATGGAGGAGAACCTCAATTCACATC	1193
QY	841	TACAACTGGAGCACCGCTGAGCTGAGCAT	GAGCCGAGTACTCTTTTACTCGGCCAGAT	900
Db	1194	TACAACTGGAGCACCGCTGAGCATGAGCC	GAGGAGTACTCTTTTACTCGGCCAGAT	1253
QY	901	GCGCTGGAGATGCTCACTTCATGAACTCG	CATCTCTTATGGAGACATGAACCTCGAG	960
Db	1254	GCGCTGGAGATGCTCACTTCATGAACTCG	CATCTCTTATGGAGACATGAACCTCGAG	1313
QY	961	AATGTGCTTCTGATGAGCCTCGAGCACTG	CAGCTTATCTGACCTGAGGAGCTGAGC	1020
Db	1314	AATGTGCTTCTGATGAGCCTCGAGCACTG	CAGCTTATCTGACCTGAGGAGCTGAGC	1373
QY	1021	ATGAAGGGTGGCAAGCCCATCACCAGAGG	CTGGAACCAATGTTTCAATGCTCTCGAG	1080
Db	1374	ATGAAGGGTGGCAAGCCCATCACCAGAGG	CTGGAACCAATGTTTCAATGCTCTCGAG	1433
QY	1081	ATCTTAATGAAAAGGTAAATTATTCCTAT	CTCTGCTGAGCTGCTTCCATGGAGACAGC	1140
Db	1434	ATCTTAATGAAAAGGTAAATTATTCCTAT	CTCTGCTGAGCTGCTTCCATGGAGACAGC	1493
QY	1141	ATTATTAATGAAATGGTTCCTGAGAGAA	CCACTTCAAAATATACAGAAAAAGCTG	1200
Db	1494	ATTATTAATGAAATGGTTCCTGAGAGAA	CCACTTCAAAATATACAGAAAAAGCTG	1553
QY	1201	GAGGATCTGAAGCAAAAGACTCTGCAAG	AGAGTCAAAATTCAGCATGTAACTTCA	1260
Db	1554	GAGGATCTGAAGCAAAAGACTCTGCAAG	AGAGTCAAAATTCAGCATGTAACTTCA	1613
QY	1261	GAGGAGCCAAAAGTATTTGAGGCTCTT	TGAGCTTCTGAGTAAAGAACAGAGCA	1320
Db	1614	GAGGAGCCAAAAGTATTTGAGGCTCTT	TGAGCTTCTGAGTAAAGAACAGAGCA	1673
QY	1321	AGCAGAGAAAAGTCTGATGATCCAGAGAA	CATCATCTTTTAAAGATCAACTTCT	1380
Db	1674	AGCAGAGAAAAGTCTGATGATCCAGAGAA	CATCATCTTTTAAAGATCAACTTCT	1733
QY	1381	CGCGTGAAGCTGGCCTAATTAATGAA	CCCCCAATTTGSCAGACCTTCAGTGT	1440
Db	1734	CGCGTGAAGCTGGCCTAATTAATGAA	CCCCCAATTTGSCAGACCTTCAGTGT	1793
QY	1441	AAAGCATCGCTGAATTAATGATTAATTC	TCTGAGGCTTCGGGGGGTGGAAATTT	1500
Db	1794	AAAGCATCGCTGAATTAATGATTAATTC	TCTGAGGCTTCGGGGGGTGGAAATTT	1853
QY	1501	GATTAAGCACTTCTTCAAAAACCTTGG	CGAGGGTCTTCTATAGCATGGCAGAGAA	1560
Db	1854	GATTAAGCACTTCTTCAAAAACCTTGG	CGAGGGTCTTCTATAGCATGGCAGAGAA	1913
QY	1561	ATTATTAAGAAACGGAGCTGTTGAGAA	CTGATGACCCCAAGACCTAAGGGTGT	1620
Db	1914	ATTATTAAGAAACGGAGCTGTTGAGAA	CTGATGACCCCAAGACCTAAGGGTGT	1973
QY	1621	GAGGGTAAATTCACCAAGTCTGAGCTGT	GCTTTGTTATG 1559	
Db	1974	GAGGGTAAATTCACCAAGTCTGAGCTGT	GCTTTGTTATG 2012	
RESULT 6				
US-10-217-745-1				
; Sequence 1, Application US/10217745				
; Publication No. US20030004328A1				
; GENERAL INFORMATION:				
; APPLICANT: Walke, D. Wade				
; APPLICANT: Wilgowski, Nathaniel L.				
; APPLICANT: Turner, C. Alexander Jr.				

RESULT 6
US-10-217-745-1
Sequence 1, Application US/10217745
Publication No. US2003000438A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
INVENTOR: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.

;; TITLE OF INVENTION: No. US20030004328A1e1 Human G-Coupled Protein Receptor Kinases an
;; TITLE OF INVENTION: Polymaleolides
;; FILE OF INVENTION: Encoding the Same
;; FILE REFERENCE: LEX-0147-USA
;; CURRENT APPLICATION NUMBER: US/10/217,745
;; PRIOR APPLICATION NUMBER: 2002-08-12
;; PRIOR FILING DATE: 2001-03-08
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 1662
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-10-217-745-1

Query Match 99.8%; Score 1655.4; DB 15; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGGCGCTTGACAACTGATGCGCAACCGCCCTACCTGCAAGGCCCG 60
Db 1 ATGTGGACATGGGGGCGCTTGAGAACTGATGCGCAACCGCCCTACCTGCAAGGCCCG 60
QY 61 AAGCCCTCGACCTGCGACAGCAAAAGCTGACAGAGGGGGGGGGGCTAGAGCTGGCCCTCC 120
Db 61 AAGCCCTCGACCTGCGACAGCAAAAGCTGACAGAGGGGGGGGGGCTAGAGCTGGCCCTCC 120
QY 121 GGGGTGACAGGGCTGGGGAGCTTCGCGCAAGAGCTGCCCTGAACCTTCCACAGCTGTGT 180
Db 121 GGGGTGACAGGGCTGGGGAGCTTCGCGCAAGAGCTGCCCTGAACCTTCCACAGCTGTGT 180
QY 181 GAGAGAGAGCCCATGGTGGCGGCTCTTCCCTGACTTCTTGACCAAGTGCACAGTCCAGTTC 240
Db 181 GAGAGAGAGCCCATGGTGGCGGCTCTTCCCTGACTTCTTGACCAAGTGCACAGTCCAGTTC 240
QY 241 CGCAAGGCGGCAACTTCTGAGAGAGCTGACAGAACTGGAGAGCTGGCCCGAGAGGAGCC 300
Db 241 CGCAAGGCGGCAACTTCTGAGAGAGCTGACAGAACTGGAGAGCTGGCCCGAGAGGAGCC 300
QY 301 ACCAAGAGAGAGGCGCTGACAGAGAGCTGGTGGCCACTTGTGAGAGTGCAGCCCGGAG 360
Db 301 ACCAAGAGAGAGGCGCTGACAGAGAGCTGGTGGCCACTTGTGAGAGTGCAGCCCGGAG 360
QY 361 AACCGGCAACCTTCTGAGAGAGCTGGCCCTGACCAAGTGCAGAGCCAGCTGAG 420
Db 361 AACCGGCAACCTTCTGAGAGAGCTGGCCCTGACCAAGTGCAGAGCCAGCTGAG 420
QY 421 GAAGAGAGAGTGGCTGACAGTGCAGTGGCGCAAGGCTGAGGCGATGAGCTTCTTGCAAG 480
Db 421 GAAGAGAGAGTGGCTGACAGTGCAGTGGCGCAAGGCTGAGGCGATGAGCTTCTTGCAAG 480
QY 481 CAGCCCTTTAAGATTCTGTGACAGCGCCCTTCTACCAAGTTCTGCAAGTTCCTGCAAG 540
Db 481 CAGCCCTTTAAGATTCTGTGACAGCGCCCTTCTACCAAGTTCTGCAAGTTCCTGCAAG 540
QY 541 TTGAGATGACCAAGTGCAGCAAGTACTGACAGTTCAGAGTTCAGAGTTCGAGGAAAGT 600
Db 541 TTGAGATGACCAAGTGCAGCAAGTACTGACAGTTCAGAGTTCAGAGTTCGAGGAAAGT 600
QY 601 GGTTTTGGGAGATGATGCTGCTCAGGTGAAAACAATGAGGAGATGATGCTGAG 660
Db 601 GGTTTTGGGAGATGATGCTGCTCAGGTGAAAACAATGAGGAGATGATGCTGAG 660
QY 661 AACTGACAAAGAGGCTGAGAAAGAGAGGCTGAGAGAGTGCCTCTTTGAGAAAG 720
Db 661 AACTGACAAAGAGGCTGAGAAAGAGAGGCTGAGAGAGTGCCTCTTTGAGAAAG 720
QY 721 GAATCTTGGAGAGAGTGAAGAGCTTTTATGCTCTTGGCTTATGCTTTGAGAGC 780
Db 721 GAATCTTGGAGAGAGTGAAGAGCTTTTATGCTCTTGGCTTATGCTTTGAGAGC 780
QY 781 AAGACCATCTGCTGCTGATGAGCTGATGATGAGGAGAGCTCAAGTTCACATC 840

Db 781 AAGACCATCTGCTGCTGATGAGCTGATGATGAGGAGAGCTCAAGTTCACATC 840
QY 841 TACAAATGGGACAGCTGGCTGACATGAGCGGATGATCTTTTACTGGCCAGATA 900
Db 841 TACAAATGGGACAGCTGGCTGACATGAGCGGATGATCTTTTACTGGCCAGATA 900
QY 901 GCCTGGAGATGCTGACCTCCCAATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 960
Db 901 GCCTGGAGATGCTGACCTCCCAATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 960
QY 961 AATGCTTCTGATGCTGACCTGCAAGTGCAGAGTTCATGCACTGGGGCTGGCCGAG 1020
Db 961 AATGCTTCTGATGCTGACCTGCAAGTGCAGAGTTCATGCACTGGGGCTGGCCGAG 1020
QY 1021 ATGAAGGCTGCAAGCCCATCAACCAAGGCTGAGAACCAATGCTGATGCTGATG 1080
Db 1021 ATGAAGGCTGCAAGCCCATCAACCAAGGCTGAGAACCAATGCTGATGCTGATG 1080
QY 1081 ATCTTAATGAAAAGTAACTTATCTTATCTGATGCTGATGCTGATGCTGATGCTGATG 1140
Db 1081 ATCTTAATGAAAAGTAACTTATCTTATCTGATGCTGATGCTGATGCTGATGCTGATG 1140
QY 1141 ATTATGAAAATGCTGCTGACAGAACCATTCATCAAGTAAAGTCACTGATA 1200
Db 1141 ATTATGAAAATGCTGCTGACAGAACCATTCATCAAGTAAAGTCACTGATA 1200
QY 1201 GAGATCTGAGAGAGAACTCTGCAAGAGAGTCAATTCAGCATGATTAATTCACA 1260
Db 1201 GAGATCTGAGAGAGAACTCTGCAAGAGAGTCAATTCAGCATGATTAATTCACA 1260
QY 1261 GAGAGAGCAAAAGATTTTGAAGGCTCTTCTGCTAAGAAACCAAGCAAGCTTGA 1320
Db 1261 GAGAGAGCAAAAGATTTTGAAGGCTCTTCTGCTAAGAAACCAAGCAAGCTTGA 1320
QY 1321 AGCAGAGAAAAGTGTGATGATCCAGAGAAACATCTTCTTAAAGATCAATCTTCT 1380
Db 1321 AGCAGAGAAAAGTGTGATGATCCAGAGAAACATCTTCTTAAAGATCAATCTTCT 1380
QY 1381 CGCTGGAAGCTGCTTATGAAACCCCATTTGTGCAAGACCTTCACTGATGATG 1440
Db 1381 CGCTGGAAGCTGCTTATGAAACCCCATTTGTGCAAGACCTTCACTGATGATG 1440
QY 1441 AAGACATGCTGATGATGATTTCTGAGGTTGGGGGCTGGAATTTGATGACAA 1500
Db 1441 AAGACATGCTGATGATGATTTCTGAGGTTGGGGGCTGGAATTTGATGACAA 1500
QY 1501 GATAGAGATTTCTCAAAAATTGCGACAGGCTGCTCTTATGCAATGAGAGAGAA 1560
Db 1501 GATAGAGATTTCTCAAAAATTGCGACAGGCTGCTCTTATGCAATGAGAGAGAA 1560
QY 1561 ATTATGAAAAGGAGCTGTTGAGAACTGAATGACCCCAAGACCTGAGGCTGAG 1620
Db 1561 ATTATGAAAAGGAGCTGTTGAGAACTGAATGACCCCAAGACCTGAGGCTGAG 1620
QY 1621 GAGGATTAATTCACAGTCTGCGGCTGCTTGTATG 1659
Db 1621 GAGGATTAATTCACAGTCTGCGGCTGCTTGTATG 1659

RESULT 7
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
; FILE REFERENCE: C1000634D1V
; CURRENT APPLICATION NUMBER: US/09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331

PRIOR FILING DATE: 2000-06-01
 PRIOR APPLICATION NUMBER: 09/738,894
 PRIOR FILING DATE: 2000-12-18
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1662
 TYPE: DNA
 ORGANISM: Human
 US-09-964-469-1

Query Match 99.7%; Score 1654.2; DB 9; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTGAGCAATGGGGGCGCTGAGCAAACTGATGCGCAACAGCGCTGACTGAGGCGCCG 60
 DB 1 ATGTGAGCAATGGGGGCGCTGAGCAAACTGATGCGCAACAGCGCTGACTGAGGCGCCG 60
 QY 61 AAGCCCTGCACTGCAAGCAAGAGCTGAGCGGCGGCGGCTGAGCGCTGAGCGCTGAGCG 120
 DB 61 AAGCCCTGCACTGCAAGCAAGAGCTGAGCGGCGGCGGCTGAGCGCTGAGCGCTGAGCG 120
 QY 61 AAGCCCTGCACTGCAAGCAAGAGCTGAGCGGCGGCGGCTGAGCGCTGAGCGCTGAGCG 120
 DB 61 AAGCCCTGCACTGCAAGCAAGAGCTGAGCGGCGGCGGCTGAGCGCTGAGCGCTGAGCG 120
 QY 121 GGGCTGCAAGGCTGCGGAGCTCGGCGCAAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 180
 DB 121 GGGCTGCAAGGCTGCGGAGCTCGGCGCAAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 180
 QY 121 GGGCTGCAAGGCTGCGGAGCTCGGCGCAAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 180
 DB 121 GGGCTGCAAGGCTGCGGAGCTCGGCGCAAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 180
 QY 181 GAGCAGCAAGCCATGCGTGGCGGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 240
 DB 181 GAGCAGCAAGCCATGCGTGGCGGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 240
 QY 181 GAGCAGCAAGCCATGCGTGGCGGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 240
 DB 181 GAGCAGCAAGCCATGCGTGGCGGCTGCTGAGAGCTGCTGAGAGCTGCTGAGAGCTGCTG 240
 QY 241 CGAGAGCGGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 300
 DB 241 CGAGAGCGGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 300
 QY 241 CGAGAGCGGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 300
 DB 241 CGAGAGCGGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 300
 QY 301 ACAGAGAGAGCGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 360
 DB 301 ACAGAGAGAGCGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 360
 QY 301 ACAGAGAGAGCGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 360
 DB 301 ACAGAGAGAGCGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 360
 QY 361 AACCCGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
 DB 361 AACCCGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
 QY 361 AACCCGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
 DB 361 AACCCGCAAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
 QY 421 GAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480
 DB 421 GAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480
 QY 421 GAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480
 DB 421 GAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480
 QY 481 CAGCCCTTGAAGAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 540
 DB 481 CAGCCCTTGAAGAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 540
 QY 481 CAGCCCTTGAAGAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 540
 DB 481 CAGCCCTTGAAGAGCTTCTTGAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 540
 QY 541 TTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 600
 DB 541 TTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 600
 QY 541 TTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 600
 DB 541 TTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 600
 QY 601 GGTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 660
 DB 601 GGTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 660
 QY 601 GGTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 660
 DB 601 GGTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 660
 QY 661 AAGCTGCAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 720
 DB 661 AAGCTGCAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 720
 QY 661 AAGCTGCAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 720
 DB 661 AAGCTGCAAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 720
 QY 721 GAAATCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 780
 DB 721 GAAATCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 780
 QY 721 GAAATCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 780
 DB 721 GAAATCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 780
 QY 781 AAGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 781 AAGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 781 AAGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 781 AAGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 841 TACAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 900
 DB 841 TACAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 900

DB 841 TACAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 900
 QY 901 GCTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 960
 DB 901 GCTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 960
 QY 901 GCTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 960
 DB 901 GCTGTTGGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 960
 QY 961 AAGTCTGCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1020
 DB 961 AAGTCTGCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1020
 QY 961 AAGTCTGCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1020
 DB 961 AAGTCTGCTGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1020
 QY 1021 ATGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1080
 DB 1021 ATGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1080
 QY 1021 ATGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1080
 DB 1021 ATGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1080
 QY 1081 ATCTGATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1140
 DB 1081 ATCTGATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1140
 QY 1081 ATCTGATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1140
 DB 1081 ATCTGATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1140
 QY 1141 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1200
 DB 1141 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1200
 QY 1141 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1200
 DB 1141 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1200
 QY 1201 GAGAGATCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1260
 DB 1201 GAGAGATCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1260
 QY 1201 GAGAGATCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1260
 DB 1201 GAGAGATCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1260
 QY 1261 GAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1320
 DB 1261 GAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1320
 QY 1261 GAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1320
 DB 1261 GAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1320
 QY 1321 AGCAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1380
 DB 1321 AGCAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1380
 QY 1321 AGCAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1380
 DB 1321 AGCAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1380
 QY 1381 GCGCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1440
 DB 1381 GCGCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1440
 QY 1381 GCGCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1440
 DB 1381 GCGCTGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1440
 QY 1441 AAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1500
 DB 1441 AAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1500
 QY 1441 AAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1500
 DB 1441 AAGAGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1500
 QY 1501 GATTAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1560
 DB 1501 GATTAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1560
 QY 1501 GATTAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1560
 DB 1501 GATTAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1560
 QY 1561 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1620
 DB 1561 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1620
 QY 1561 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1620
 DB 1561 ATTATGAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 1620
 QY 1621 GAGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1659
 DB 1621 GAGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1659

RESULT 8
 US-10-425-962-1
 Sequence 1, Application US/10425962
 Publication No. US20030180786A1
 GENERAL INFORMATION:
 APPLICANT: GUSEL, Karl et al
 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: C1000636D1V2
 CURRENT APPLICATION NUMBER: US/10/425,962
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 09/964,469
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: 09/738,894
 PRIOR FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: 60/208,331
 PRIOR FILING DATE: 2000-06-01

QY 1 ATGCTGACACTGCGGCGCCCTTGAGCAACTGATGCGCAACACGCGCTACCTGACGCGCCG 60
Db 1 ATGCTGACACTGCGGCGCGCCCTTGAGCAACTGATGCGCAACACGCGCTACCTGACGCGCCG 60
QY 61 AAGCCCTCGGACCTGCGACAGCAAAAGGCTGACGCGCGCGCGCTGAGCTGAGCTGCGCC 120
Db 61 AAGCCCTCGGACCTGCGACAGCAAAAGGCTGACGCGCGCGCGCGCTGAGCTGAGCTGCGCC 120
QY 121 GGGCTGCAAGGCTGCGCGAGACTCGCGACGAGCTGCGCTGCAACTTCCAGACTGCTGCT 180
Db 121 GGGCTGCAAGGCTGCGCGAGACTCGCGACGAGCTGCGCTGCAACTTCCAGACTGCTGCT 180
QY 181 GAGCAGCAGCAGCCATGCGCTGCGCTCTCTTCTGTACTTCTGACAGTAGTCCCAAGCTTC 240
Db 181 GAGCAGCAGCAGCCATGCGCTGCGCTCTCTTCTGTACTTCTGACAGTAGTCCCAAGCTTC 240
QY 241 CGAAGAGCGGACCTTCTCTAGAGGACCTGAGAACTGAGAGCTGCGCGAGAGAGAGCC 300
Db 241 CGAAGAGCGGACCTTCTCTAGAGGACCTGAGAACTGAGAGCTGCGCGAGAGAGAGCC 300
QY 301 ACCAAGAAGACGCGCTGCGAGGCGCTGAGCCACTTTGTGCGAGTGCGCCCGCGCGG 360
Db 301 ACCAAGAAGACGCGCTGCGAGGCGCTGAGCCACTTTGTGCGAGTGCGCCCGCGCGG 360
QY 361 AACCGGCAACCTTCTCTGACGAGCGCTGCGCAACAAGTGCAGAGCAACAATGAG 420
Db 361 AACCGGCAACCTTCTCTGACGAGCGCTGCGCAACAAGTGCAGAGCAACAATGAG 420
QY 421 GAAGAGCAGAGTGCCTGACAGTAGAGCTGCGCAAGGCTGAGGCCATGCGCTTCTTGAGAG 480
Db 421 GAAGAGCAGAGTGCCTGACAGTAGAGCTGCGCAAGGCTGAGGCCATGCGCTTCTTGAGAG 480
QY 481 CAGCCCTTTAAGATTTCTGACAGCGCGCTTCTAGACAAAGTTCTGCGAGTGAAGATC 540
Db 481 CAGCCCTTTAAGATTTCTGACAGCGCGCTTCTAGACAAAGTTCTGCGAGTGAAGATC 540
QY 541 TTGCGAGTGCACCAAGTGCACAGCAAGTCTTCACTGAGTTCAGAGTGCAGGAAAGT 600
Db 541 TTGCGAGTGCACCAAGTGCACAGCAAGTCTTCACTGAGTTCAGAGTGCAGGAAAGT 600
QY 601 GGTGTTTGCGAGTATGTCGCGCTCAGGTGAAGAAACAATGAGAGATGATATGCTGAG 660
Db 601 GGTGTTTGCGAGTATGTCGCGCTCAGGTGAAGAAACAATGAGAGATGATATGCTGAG 660
QY 661 AAATCTGACAAAGGCGGCTGAAGAAAGAGTGGCGAAGATGCGCTCTTTGGAAAG 720
Db 661 AAATCTGACAAAGGCGGCTGAAGAAAGAGTGGCGAAGATGCGCTCTTTGGAAAG 720
QY 721 GAAATCTTGGAGAAAGTCAAGCAGCGCTTCTATTTGCTCTGCGCTATAGCTTTGAGAGC 780
Db 721 GAAATCTTGGAGAAAGTCAAGCAGCGCTTCTATTTGCTCTGCGCTATAGCTTTGAGAGC 780
QY 781 AAGACCATCTGCGCTTGTATGAGGCTGATGAATGAGGGGAGACCTCAAGTTCCATATC 840
Db 781 AAGACCATCTGCGCTTGTATGAGGCTGATGAATGAGGGGAGACCTCAAGTTCCATATC 840
QY 841 TACAACTGAGGACGCGCTGAGCATGAGCCGAGTGAATCTTTTACTCGGCGCAAGTA 900
Db 841 TACAACTGAGGACGCGCTGAGCATGAGCCGAGTGAATCTTTTACTCGGCGCAAGTA 900
QY 901 GCTGTGGAATGCTGACCTTCATGAACTTCGCGATTCGTATGCGGACATGAAAGCTGAG 960

Db	901	GCCTGGGAGT	GCTGACCTTCCTCA	TGAACCTGGCA	TCGTCTATCGGGACATGA	AGCTTGAG	960
QY	961	AATGTGCTTCTG	ATGACCTCGCA	CTGCACTGCA	GGTATTCTGA	CTTGGGGCGTGGCGCTGGAG	102
Db	961	AATGTGCTTCTG	ATGACCTCGCA	CTGCACTGCA	GGTATTCTGA	CTTGGGGCGTGGCGCTGGAG	102
QY	1021	ATGAAAGGGTGG	CAACCCCATATCA	CCCAAGAGGCTG	GAACCAATGGTTA	CATGCTCTTGAG	108
Db	1021	ATGAAAGGGTGG	CAACCCCATATCA	CCCAAGAGGCTG	GAACCAATGGTTA	CATGCTCTTGAG	108
QY	1081	ATCTTAATGGA	AAAAAGTAA	GTATTCTTCAT	CTCTGGTGA	ATGGSTTTGGCATGGGATGCA	114
Db	1081	ATCTTAATGGA	AAAAAGTAA	GTATTCTTCAT	CTCTGGTGA	ATGGSTTTGGCATGGGATGCA	114
QY	1141	ATTATTGA	ATGGTTGCTG	GAACGA	CACATTTCA	AGATTACAAGAAAAAGTCA	120
Db	1141	ATTATTGA	ATGGTTGCTG	GAACGA	CACATTTCA	AGATTACAAGAAAAAGTCA	120
QY	1201	GAGGATCTGA	ACAAAGAACTT	CTGGCAACGA	AGGTCAATTTCA	GCATGATTA	126
Db	1201	GAGGATCTGA	ACAAAGAACTT	CTGGCAACGA	AGGTCAATTTCA	GCATGATTA	126
QY	1261	GAGGAAACAAA	GAATATTG	TGCAAGGCTCTT	CTTGAGTAA	ACCAAGGCA	132
Db	1261	GAGGAAACAAA	GAATATTG	TGCAAGGCTCTT	CTTGAGTAA	ACCAAGGCA	132
QY	1321	AGCAGAAAAA	AGTCTGA	TATCCACG	AAAAATCATATTTCTTTAA	ACATCACTTCC	138
Db	1321	AGCAGAAAAA	AGTCTGA	TATCCACG	AAAAATCATATTTCTTTAA	ACATCACTTCC	138
QY	1381	CGCCTGGAG	AGCTGGCTTA	ATTTGA	CCCCCATTTGG	CCAGACCTTCA	144
Db	1381	CGCCTGGAG	AGCTGGCTTA	ATTTGA	CCCCCATTTGG	CCAGACCTTCA	144
QY	1441	AAAGACATG	CTGA	AAATTA	ATATTTCTGA	AGGTTGGGAGGAGTGA	150
Db	1441	AAAGACATG	CTGA	AAATTA	ATATTTCTGA	AGGTTGGGAGGAGTGA	150
QY	1501	GATPAGAGT	CTTCAAAA	CTTTGGCA	AGGTCGTCTT	CTATAGCATG	156
Db	1501	GATPAGAGT	CTTCAAAA	CTTTGGCA	AGGTCGTCTT	CTATAGCATG	156
QY	1561	ATTATGAAA	CGGACCTG	TTTGA	AGGAATG	ATGACCCCA	162
Db	1561	ATTATGAAA	CGGACCTG	TTTGA	AGGAATG	ATGACCCCA	162
QY	1621	GAGGGTAAT	TATCA	CCAGTCTG	AGCTGTGTT	GTATTG	168
Db	1621	GAGGGTAAT	TATCA	CCAGTCTG	AGCTGTGTT	GTATTG	168

Db 439 GAAAGCGAGATGACCTGACGATGACCTGCGCCAAAGCGCTAGAGCCATGCTTTCTTGGCAAGAG 498

Qy 481 CAGCCCTTTAAGGATTTGTGACCAAGCGCTTTCTTACGACAAGATTTCTGCGATGGAAAATCC 540

Db 499 CAGCCCTTTAAGGATTTGTGACCAAGCGCTTTCTTACGACAAGATTTCTGCGATGGAAAATCC 558

Qy 541 TTGAGATGCAACCGATGTGACCAAGATGCTTCACTGAGTTCAAGATGCTGGGAAAGGT 600

Db 559 TTGAGATGCAACCGATGTGACCAAGATGCTTCACTGAGTTCAAGATGCTGGGAAAGGT 618

Qy 601 GATTTTGGGAGGTATGTGCGCTTCCAGGTGAAAAACACTGGAAAGATGATATGCTGTAAAG 660

Db 619 GATTTTGGGAGGTAT-----AAAAACACTGGAAAGATGATATGCTGTAAAG 663

Qy 661 AAATCGACAAAGACGCGCTGAGAAAGAAAGGTGGCGCAAGAAATGGCTCTGTGGAAAAG 720

Db 664 AAATCGACAAAGACGCGCTGAGAAAGAAAGGTGGCGCAAGAAATGGCTCTGTGGAAAAG 723

Qy 721 GAAATCTTGAAGAAGGTACAGAGCCCTTCAATGTGCTCTGTGCGCTAAGCTTTGAGAGC 780

Db 724 GAAATCTTGAAGAAGGTACAGAGCCCTTCAATGTGCTCTGTGCGCTAAGCTTTGAGAGC 783

Qy 781 AAGACCCATCTGACCTTGATGATGAGCGCTGATGATGGGGAGAACCTCAAGTTCCACATC 840

Db 784 AAGACCCATCTGACCTTGATGATGAGCGCTGATGATGGGGAGAACCTCAAGTTCCACATC 843

Qy 841 TACAACGTGGGACAGCGGTGGCTTGACATGAGCGGGGTGATCTTTTAACTCGGCCCAAGTA 900

Db 844 TACAACGTGGGACAGCGGTGGCTTGACATGAGCGGGGTGATCTTTTAACTCGGCCCAAGTA 903

Qy 901 GCGCTGGGATGCTGACCTTCATGAACCTGCGATCGCTATGCGGACATGAAGAGCTGAG 960

Db 904 GCGCTGGGATGCTGACCTTCATGAACCTGCGATCGCTATGCGGACATGAAGAGCTGAG 963

Qy 961 AATGTGCTTGGATGACCTCGGCAATGCAAGGTTATCTGACCTGGGGCTGGCGGTGAG 1020

Db 964 AATGTGCTTGGATGACCTCGGCAATGCAAGGTTATCTGACCTGGGGCTGGCGGTGAG 1023

Qy 1021 AATGAAGGTGGCAAGCCCATCCCAAG---GGCTGAACAAATGGTTAAATAGGCTCTC 1077

Dd	1024	ATGAAGGGATGGCAAGCCCACTCAACCCAGAGGACAGGCTGGAAACCAATGGTTAAATAGTGCCTCT	1083
Qy	1078	GAGATCTTAAGGAAAAGGTAAAGTTATTCCTATCTGTGACCTGGTTGGCATGGGAATGC	1137
Dd	1084	GGAATCTTAATGAAAAGGTAAAGTTATTCCTATCTGTGACCTGGTTGGCATGGGAATGC	1143
Qy	1138	AGCATTTATGAAATAGGTGTCTGACGAAACCACTCAAGATTTACAAGAAAAGTCAGT	1197
Dd	1144	AGCATTTATGAAATAGGTGTCTGACGAAACCACTCAAGATTTACAAGAAAAGTCAGT	1203
Qy	1198	AAAGAGATCTGAACGAAAGAACTCTGACAGAGAGGTCAAAATTCACGATGATTAATCTC	1257
Dd	1204	AAAGAGATCTGAACGAAAGAACTCTGACAGAGAGGTCAAAATTCACGATGATTAATCTC	1263
Qy	1258	ACGAGAGAAAGCAAAAGATATTTGACAGCTCTTCTGGCTAATAAACAAGCAAGCAAGCTTA	1317
Dd	1264	ACGAGAGAAAGCAAAAGATATTTGACAGCTCTTCTGGCTAATAAACAAGCAAGCAAGCTTA	1323
Qy	1318	GGAAGC---AGAGAAAAGTCTGATGATCCGAGAAACATCATTTCTTTAAAAAGATCAAC	1374
Dd	1324	GGAAGAGAGAGGAAAAGTCTGATGATCCGAGAAACATCATTTCTTTAAAAAGATCAAC	1383
Qy	1375	TTTTCTCGCTGGGAAAGCTGGCGCTTAATTGAACCCCACTTGTGTCACAGACCTTCAGTGGTT	1434
Dd	1384	TTTTCTCGCTGGGAAAGCTGGCGCTTAATTGAACCCCACTTGTGTCACAGACCTTCAGTGGTT	1443
Qy	1435	TATSCAAAGACATGCTGTAATTTGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGAT	1499
Dd	1444	TATSCAAAGACATGCTGTAATTTGATGATTTCTCTGAGGTTTCGGGGGGTGGAAATTTGAT	1507
Qy	1495	GACAAAGATTAACGATTTCTTCAAAAACCTTGGGACAGGTCTGTTCTATAGCATGGCAG	1554

Db 1504 GACAAAGATAGAGTCTTCTCAAACTTTGCGAGAGTCTGTCTCTATAGCATGCGAG 1563
 QY 1555 GAGAAATTATGAAAGCGGACTGTTTGAGAACTGATGATACCCCAAGACTTACGGGT 1614
 Db 1564 GAGAAATTATGAAAGCGGACTGTTTGAGAACTGATGATACCCCAAGACTTACGGGT 1623
 QY 1615 TGTGAGAGAGGTAATTATCATCGAGTCTGCGGTGTGTATG 1659
 Db 1624 TGTGAGAGAGGTAATTATCATCGAGTCTGCGGTGTGTATG 1668

RESULT 10
 US-10-217-745-3
 ; Sequence 3, Application US/10217745
 ; Publication No. US2003004328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. US2003004328A1 Human G-Coupled Protein Receptor Kinases and
 ; TITLE OF INVENTION: Polynucleotides
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; PRIOR FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: US/09/802,117
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-217-745-3

Query Match 63.1%; Score 1046.8; DB 15; Length 1062;
 Best Local Similarity 99.8%; Pred. No. 3.8e-312;
 Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGTGACATGCGGCGCTTGACAACTGATGCCCAACACCGGCTACTGAGCGCGG 60
 Db 1 ATGTGTGACATGCGGCGCTTGACAACTGATGCCCAACACCGGCTACTGAGCGCGG 60
 QY 61 AAGCCCTGACGCTGCGACGAAAGAGCTGACGCGCGCGCGCTGAGCCTTGGCC 120
 Db 61 AAGCCCTGACGCTGCGACGAAAGAGCTGACGCGCGCGCGCTGAGCCTTGGCC 120
 QY 121 GGGCTGAGAGGCTGCGCGAGCTCGCGACAAAGCTGTCCCTGAACTTCCACAGCTGT 180
 Db 121 GGGCTGAGAGGCTGCGCGAGCTCGCGACAAAGCTGTCCCTGAACTTCCACAGCTGT 180
 QY 181 GAGCAGCAGCCATGCTGTGCGGCTCTTCCGTGACTTCTAGCCACAGTGCACGTTT 240
 Db 181 GAGCAGCAGCCATGCTGTGCGGCTCTTCCGTGACTTCTAGCCACAGTGCACGTTT 240
 QY 241 CGCAAGGCGGCACTCTTCTAGAGAGCTGCAAACTGGAGCTGTGCGCGACGCGCC 300
 Db 241 CGCAAGGCGGCACTCTTCTAGAGAGCTGCAAACTGGAGCTGTGCGCGACGCGCC 300
 QY 301 ACCAAAGACGCGCTGCGAGGCGTGTGCGCACTTGTGTGAGTGCCTTCCCGCGG 360
 Db 301 ACCAAAGACGCGCTGCGAGGCGTGTGCGCACTTGTGTGAGTGCCTTCCCGCGG 360
 QY 361 AACCCGCACTCTTCTGAGCGAGCGGTGCGCAAGTGTCCAGACGACCACTGAG 420
 Db 361 AACCCGCACTCTTCTGAGCGAGCGGTGCGCAAGTGTCCAGACGACCACTGAG 420
 QY 421 GAAAGCGAGTGTGCGAGTGTGCGCGAGTGTGCGCGAGTGTGCGCGAGTGTGCGAG 480
 Db 421 GAAAGCGAGTGTGCGAGTGTGCGCGAGTGTGCGCGAGTGTGCGCGAGTGTGCGAG 480
 QY 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGTGTGTGAGTGAAGCT 540
 Db 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGTGTGTGAGTGAAGCT 540

Db 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGTGTGTGAGTGAAGCT 540
 QY 541 TTGAGAGTGAACCACTGTGAGCAAACTACTTACTGATGATGCTGCGGAAAGT 600
 Db 541 TTGAGAGTGAACCACTGTGAGCAAACTACTTACTGATGATGCTGCGGAAAGT 600
 QY 601 GGTTTTGGGAGTATGTGCGGTGAGTGAAGAACTCTGAGAAATGATGCTGTAG 660
 Db 601 GGTTTTGGGAGTATGTGCGGTGAGTGAAGAACTCTGAGAAATGATGCTGTAG 660
 QY 661 AAATCTGACAAAGGCGCTGAGAAAGTGTGCGAGAAAGATGCTCTTGGAAAG 720
 Db 661 AAATCTGACAAAGGCGCTGAGAAAGTGTGCGAGAAAGATGCTCTTGGAAAG 720
 QY 721 GAAATCTTGAAGAGTCAAGCGCTTCAATGCTGTCTGCGCTATGCTTTGAGAGC 780
 Db 721 GAAATCTTGAAGAGTCAAGCGCTTCAATGCTGTCTGCGCTATGCTTTGAGAGC 780
 QY 781 AAGACCATCTGCTGCTGTGATGAGCTGATGAATGCGGAGAGACTCAAGTTCACATC 840
 Db 781 AAGACCATCTGCTGCTGTGATGAGCTGATGAATGCGGAGAGACTCAAGTTCACATC 840
 QY 841 TACACGTGCGCAGCGCTGCTGAGCATGAGCGCGGTGATCTTTTACCTGCGCCAGATA 900
 Db 841 TACACGTGCGCAGCGCTGCTGAGCATGAGCGCGGTGATCTTTTACCTGCGCCAGATA 900
 QY 901 GCGTGTGAGTGTGCTGACCTTCCATGAACTGCGCATCTTATGCGACATGAGCTGAG 960
 Db 901 GCGTGTGAGTGTGCTGACCTTCCATGAACTGCGCATCTTATGCGGAGCATGAGCTGAG 960
 QY 961 AATGTCTTCTGATGACCTGCGCACTGCAAGTGTATCTGACTGCGGCTGCGGAG 1020
 Db 961 AATGTCTTCTGATGACCTGCGCACTGCAAGTGTATCTGACTGCGGCTGCGGAG 1020
 QY 1021 ATGAGGCTGTGCGAAGCCCATCACCGAGG 1050
 Db 1021 ATGAGGCTGTGCGAAGCCCATCACCGAGG 1050

RESULT 11
 US-09-964-469-3
 ; Sequence 3, Application US/09964469
 ; Patent No. US20020034803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIBLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: C1000636DIV
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1) - (36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-964-469-3

Query Match 37.2%; Score 617.4; DB 9; Length 36651;
 Best Local Similarity 96.8%; Pred. No. 1.5e-178;
 Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTGTGACATGCGGCGCTTGACAACTGATGCCCAACACCGGCTACTGAGCGCGG 60
 Db 1 ATGTGTGACATGCGGCGCTTGACAACTGATGCCCAACACCGGCTACTGAGCGCGG 60

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Query Match      37.2%; Score 617.4; DB 15; Length 36651;
Best Local Similarity 96.8%; Pred. No. 1.5e-178;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      1  ATGTGTGACATATGGGGGGCCCTGTGACAACTTGATGTGCMAACACGGCTTACCTTGACAGTCCCG 60
Db      2076  ATGTGTGACATATGGGGGGCCCTGTGACAACTTGATGTGCMAACACGGCTTACCTTGACAGTCCCG 2135

QY      61  AACCCCTTGACACTGCCACACGAAAGAGCTGTGAGGGGGGGGGGGGGAGCTTGAGCCCTTGCC 120
Db      2136  AACCCCTTGACACTGCCACACGAAAGAGCTGTGAGGGGGGGGGGGGGAGCTTGAGCCCTTGCC 2195

QY      121  GGGCTGACAGAGCTCGCGAGCTCCGCCAGAGAGCTGTCCCTGAACTTTCACACAGCTGTGT 180
Db      2196  GGGCTGACAGAGCTCGCGAGCTCCGCCAGAGAGCTGTCCCTGAACTTTCACACAGCTGTGT 2255

QY      181  GAGCAGACACCCCATGTGTGCGCGCTCTTCCCTGTACCTTCTTAGCCACAGTGTCCACGTTG 240
Db      2256  GAGCAGACACCCCATGTGTGCGCGCTCTTCCCTGTACCTTCTTAGCCACAGTGTCCACGTTG 2315

QY      241  CGAAGAGGGGCAACCTTCTTAGAGACGTGACGAATCGGAGAGCTGGCCGAGAGGACCC 300
Db      2316  CGAAGAGGGGCAACCTTCTTAGAGACGTGACGAATCGGAGAGCTGGCCGAGAGGACCC 2375

QY      301  ACCAAAGACAGCGCGCTGTGACAGGGCTGTGTGCACATTGTGCGAGTCCCTTGCCCGGG 360
Db      2376  ACCAAAGACAGCGCGCTGTGACAGGGCTGTGTGCACATTGTGCGAGTCCCTTGCCCGGG 2435

QY      361  AACCCGCAACCTTCTTCACGACGAGCGCGGGCACCAAGTGTGCACACACACACACTAG 420
Db      2436  AACCCGCAACCTTCTTCACGACGAGCGCGGGCACCAAGTGTGCACACACACACACTAG 2495

QY      421  GAAAGCGAGTGGCTGTGACGTGTGCGCAAGGTGAGGCGCATGTCTTCTTGACAG 480
Db      2496  GAAAGCGAGTGGCTGTGACGTGTGCGCAAGGTGAGGCGCATGTCTTCTTGACAG 2555

QY      481  CAGCCCTTTAAAGATTGTGTGACCAAGCGCTTCTTACGACAAGTTTGTGAGGGAATC 540
Db      2556  CAGCCCTTTAAAGATTGTGTGACCAAGCGCTTCTTACGACAAGTTTGTGAGGGAATC 2615

QY      541  TTGAGAGTGAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTGTGGGAAAAGT 600
Db      2616  TTGAGAGTGAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAGAGTGTGGGAAAAGT 2675

QY      601  GATTTTGGGAGGTATGTGCCGTTCAGGTGAAAACACTGTGAAAAGATGAT 651
Db      2676  GATTTTGGGAGGTATGTGCCGTTCAGGTGAAAACACTGAAAGTGAAGCAT 2726

RESULT 13
US-09-851-686-2
; Sequence 2, Application US/09851686
; Patent No. US20020034767A1
; GENERAL INFORMATION:
; APPLICANT: Gomez, Jorge
; APPLICANT: Benovic, Jeffrey L.
; APPLICANT: Kumapalli, Priya
; TITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein
; TITLE OF INVENTION: Receptor Kinases GRK5 and GRK6
; FILE REFERENCE: JEFF-0118-DIV
; CURRENT APPLICATION NUMBER: US/09/851,686
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 08/464,954
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/076,084
; PRIOR FILING DATE: 1993-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-851-686-2

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QY 15 GGCCTCGAGCAACTGATGCGCAACCCGCTTACTGTGAGGCCCGGAGAGCCTTGAGACTG 74
 Db 65 GGGAGCTCGAGGAACATGCTGAGCGACACAGGTATCTACAGGCCCCGGAGAGAGGTGGCGGTGG 12
 QY 75 CGACAGCAAAAG--AGGTGACACGGCGCGGGGTAGCTGGCCCTTGCCTCGAGGG 13
 Db 125 AATATGCGAAAGGCAAAAGCAGAGAAATGGCGGAGATGGCTCAAGTTCTCCACATCAAGCCA 184
 QY 132 CTGCGCGAAGCTTCGCGCAGAAAGCTGTCCCTGAACTTCCAGAGCTGTGTGAGCAGAGCGC 191
 Db 185 GTGCGAAGAGCTGGGCTCAGCTTCGAGGTGTACTATTCAGAGCTGTGTGAGCGGAGCGC 244
 QY 192 CATGSGTGGCGGCTCTTTCCTGTACTTTCAGCCACAGTCCCAAGTCCTCGCAGAGCGCG 251
 Db 245 CATTTGGCGGCTGTCTGTTCAGAGTGTGTGTCCACAGAGCGCGAGGTGAGCGGTGGCT 304
 QY 252 AACCTTCTAGAGAGAGTGTGAGAACTGTGAGGTGGCGGAGAGAGAGACCCAGCAAAAGACAG 311
 Db 305 CGCCTTCTCGGATGGGGGTGGCGAGTATGATATACCCCGGATGACAAAGCGAGAGCATG 364
 QY 312 CGCGCTGAGGGGCTGTGTGCACTTGTGCGAGTGGCCCTGGCGGAGAACCGCAAC 371
 Db 365 TGGGGGAGAG--TAAAGCAAAATTTCTGAGCACAAGGATCTTGACCTCATCTCGA 421
 QY 372 CTYTCTAGCAGAGCGCGGTGCGCACAGAGGCGCAGAGCCACATGAGAGAGCGAGT 431
 Db 422 GGTCCCCCGGAGCTGTGTGAGAAC--TGCACCGAGCGGTGAGAGAGGTCTCCCTCAAG 480
 QY 432 GCGCTGAGTACGCTGGCGAAAGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTAA 491
 Db 481 ACCTTTTCCAGAACTCAACCGGCTGA--CCAGAGATACGTAGCGTGGCCCTTTTGC 538
 QY 492 GGAATTTGATACAGAGGCTTTTACGACAAAGTTTGTGCGAGAACTTTGAGANTCA 551
 Db 539 GCACTACTTGAGAGCATCTTACCTTCAACCGTTTCTGCGAGTGAAGTGGCTGGAAAGCA 598
 QY 552 ACAGGTGTCAAGAAAGTACTTTCATGAGTGTGCGAGGTGCGGAGAAAGTGTGTTTGGGA 611
 Db 599 GCGAGTGACCAAAAACACTTTCAGGAGATACCGAGTCTGTGGCAAAAGTGGCTTTGGGGA 658
 QY 612 GGTATGTGCGCTCGAGGTGAAAAACCTGGAGAGATGTATGCTGTAGAACTGTGACAA 671
 Db 659 GGTGTGGGCTCCCGAGGTGGGCGCACAGGTAAAGATGTGCTGTGCAAGACCTAGGAA 718
 QY 672 GAACGCGCTGAAGAAAGATGTGCGAGAAATGTGCTCTTTGGAAAGAAATTTTGA 731
 Db 719 AAACGGAATCAAGAGGGGAAAGGAGAGGCAATGGGCTGTGAACAGAGACCAATCTCGGA 778
 QY 732 GAAAGTACAGAGCCCTTTCATGTGTCTCTGGGCTATGCTTTGAGAGCAAGACCAATC 791
 Db 779 GAAAGTGAACAATAGGTTTGTAGTGAAGCTTGGCTTACGCTATGAGACCAAGAGCGGCT 838
 QY 792 CTGCGTTTGCATGAGGCTGTGAATGAGAGGAGAGCTCAAGTTTCAATTTACAGTGG 851
 Db 839 GTGCGTGTGTGTGACATGATGAACGGGGGAGCCTCAAGTTTCAATCTTCCACATGG 898
 QY 852 CAGCGGTGCGCTGAGCATGAGCCGGGTGATCTTTTACCTGGCGCAGATGTGCTGTGAGAT 911
 Db 899 CCAAGGTGCTTCCCGAAGCGCGGGCGGCTTCTTACGCGCGGAGATTTGCTGTGGCT 958
 QY 912 GGTGACGCTTCATGAATCGGGAATGTCTTATGGGGAATGAAGCTTGAAGATGTGCT 971
 Db 959 GAGAGACCTTGACCGGAGAGCATGTGTACAGGAGACCTGAACCCGAGAACTATTTGCT 1018
 QY 972 GAATGACCTTGGCAATGAGAGTTATCTGACCTGGAGGTGGCGGTGAGAGAAAGGTGG 1031
 Db 1019 GGAATGACCAACGGGCATATCGGATCTCTGACTGTGAGAACTTAACTGTGCAATGTGCCAGAG 1078

QY	1032	CAAGCCATACCCAGAGGGCTGAAACCAATGGTTACATGCTCTTGAGATCTTAATGGA	1091
Db	1079	CCAGACCATTAAGAGGACGTGTGGGACACGTGGGTTCATGTGCTCCGAG--GTGGTGA	1133
QY	1092	AAAGGTAAGTATTCTCATCTCTGTGACCTGGTTTGGCANTGGGATGCAAGCATTTTAAAT	1155
Db	1136	GAATGAAACGTACACGTTCACGCTTGACTGTGTGGGGCTCGAGCTCTCTGTACGAGAT	1199
QY	1152	GGTTGCTGAGCAACACCATTTCAAGATTACAAGAAAAAGTCAGTAAAGACATCTGAA	1211
Db	1196	GATCACAGGCGAGTGTGCCCTTCAGACAGAGGAAAGAAAGATCAAGCGGAGAGGTGGA	1255
QY	1212	GCAAGAAGCTCTGCAACACAGTGTAAATTCACAGCATGAATCTTACAGAGAACGAA	1271
Db	1256	GGGCTGTGGTGAAGAGGTGTCCCGAGAGTATTCGAGCGATTTTCCCGCAGGCCGCTC	1315
QY	1272	AGATATTTGACAGGCTCTTCTGGCTTAAGAAACGAGAGCAAGCTTATAGAAAGAGAAAA	1331
Db	1316	ACTTGTCTACAGCTCTCTCTGCAAGAACCTTCGACGAAGCTGTGGGTGTCTGTGGGCGAG	1375
QY	1332	GTCTGATGATCCACAGAAACATCATTTCTTTAAAAGATCACTTCTCGCTGTGAAGC	1391
Db	1376	TGCCCGGAGGTGAAGAGACACCCGCTTTTAAAGAAAGTGAACCTTCAAGCGCTGGGAGC	1433
QY	1392	TGGCCTAATGACACCCCATTTGTGTGCCACAGCCCTTCACTGGTTTATGCCAAAGCATGCG	1451
Db	1436	TGGCAGCTGAGAGCGCGCTGTCAAGCTGACCCCGACGCCAATTTATCTGCAAGATGGTCT	1495
QY	1452	TGAATTGATGATTTCTTGAAGTTTCGGGGGTGGGAATTTGATGACAAAGATMAAGAGTT	1511
Db	1496	GACACTTTGAACAGTTCTTCAAGCTTCAAGGCGGTGAGACTGAGACCTTACCGACACGACGTT	1555
QY	1512	CTTCAAAAACCTTTGCAACAGGTGCTGTTCTTAATGACATGCAAGAAAGAAATTTATGAAC	1571
Db	1556	CTACACGAAGTTTGCACAGGACGTGGCCCATTCCTCCGCAACAGAAAGTGTGAGAC	1615
QY	1572	GGAACATGTTTGAAGAACGATGATGAC	1596
Db	1616	CGAGTCTTCCAGAACTGAAATGTC	1640

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RESULT 14
US-09-873-367C-142
; Sequence 142, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Andrews, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-873-367C-142

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Query Match	25.2%	Score 418.2	DB 10	Length 2848
Best Local Similarity	56.2%	Prid. No. 11e-117		
Matches	890	Conservative 0	Mismatches 693	Indels 12
				Gaps 5
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Db	65	GGAGCTGGAGAACATCTGATAGGAAACAAGGTGTCTACTCAAGGCCCGGAAAGGTGGCGATG	124	
Qy	75	CGACAGCAAG--AGCTGCAAGCGGCGGCGGTGACCTTGGCCCTTCCCGGCTGGACGG	131	
Db	125	AAATTCGAAAGGCAAAACAGAAATGGCGGAGATGCTCCAGAGTTCCCTCAATCAGCCA	184	
Qy	132	CTGCGCGAGACTCCCGCAAGAGCTGTCCCTGAACCTCCACAGCTCTGTGTAGCAGAGCC	191	
Db	185	GTGGGAAAGACTGCGCTCAAGCTTCAGGTGACTATCAAGCTCTTGGACCGGACCGC	244	
Qy	192	CATCGGTGCGCGCTTCTCCGTGACTTCTTACGCCACAGTGTCCACGTTCCGCAAGCGCG	251	
Db	245	CATTGGGCGCTGTCTCTTCCAGAGTTCTGTGTCCACAGAGCCGAGACTGAGCGCTGCT	304	
Qy	252	AACCTTCTTGAAGAGCTGCAAGAACTGGAGCTGGCCGAGAGAGGACCCACCAAGACAG	311	
Db	305	CGCTTCTTGAAATGGGGATGGCCGAGATGAGTGAACCCCGAATGACAGCGGAGGAGT	364	
Qy	312	CGCGCTGACGGGCTGTGTGCCACTTGTGAGATGCCCTTGGCCCGGGGAAACCCGCAAC	371	
Db	365	TGGGGGGCAGG--TAAAGCAGAAATTTTCTGAGCCACACAGGGTCTGACCTATCCTGA	421	
Qy	372	CTTCTCAGCCAGGCGCTGTGCGCAACTGTGAGATGCCCTTGGCCCGGGGAAACCCGCAAC	431	
Db	422	GGTCCCCCGGACCTGTGTGCAAG--TGCACCGAGGGCTGTGACAGGGTCCCTGCAAG	480	
Qy	432	GGCTCAGATGACCTGTGCGAAGCTGAGGCTGAGGCTTCTTGGAGAGACACCTTTAA	491	
Db	481	ACCTTTTCAAGAACTCACCCGCGCTGA--CCACAGATGACTGAGCGTGTGCCCTTTTGC	538	
Qy	492	GGATTTGCTGACAGAGGCTTCTTACAGCAAGTTTTCGAGTGGAACTCTTGAATGCA	551	
Db	539	CGACTACTCGACAGATCTTCTTACCGTTTCTGACGTGGAAGTGGCTGGAAAGCA	598	
Qy	552	ACCAAGTGCAGACAGATCTTCACTGAGTTCAAGATGCTGGGAAAGTGTTTTGGGGA	611	
Db	599	GCCAGTGCACAAAAACCTTCAAGGCAATACCAAGTCTTGGGCAAAAGTGTGGGGGA	658	
Qy	612	GGTATGTCCGTTCAGGTGAAAAACACTGGGAAAGATGTATGTCTGTAAAGAACTGGA	671	
Db	659	GGTGTGCGCTGCCAGGTGTGGGCGCACAGTAAAGTATGTGCTGCAAGAAAGCTGAGAA	718	
Qy	672	GAAAGGCTGAAAGAAAGAAAGTGTGGAGAAATGTGCTCTTGGAAAGGAAATCTTGG	731	
Db	719	AAAGCGATTCAGAAAGGAGAAAGGAGGAGGACATAGGCGCTGAACAGAAAGCATCTG	778	
Qy	732	GAAAGTGCAGAGCCCTTCAATGTCTCTGTGGCTATAGCTTGTGAGCAAGACCCATCT	791	
Db	779	GAAATGAAACAGTAGTGTGTGTATGAGCTTGTGGCTTACGCTATGAGAACAAAGACGCG	838	
Qy	792	CTGCTTGTCAATGAGCTGATGATGGGGGAGACTTGAAGTTTCAATCTTCAACAGTGG	851	
Db	839	GTGCTGTGTGCTGACATGATGAAAGGGGGGAGACTCAAGTTTCCACATCTTACACATGG	898	
Qy	852	CAGCGCTGCTGCAATGAGCGGGGTATCTTTTACTCGGCGCCAGATAGCGCTGGGAT	911	
Db	899	CGAGGCTGGCTTCCCGAAGCGGCGCGCTCTTTTACGCGCGGAGATCTGTGTGGCT	958	
Qy	912	GCTGCACCTCCATGAACTCGGCATCGTCTTATCGGACATGAAGCCTGAAATGTGCTTCT	971	
Db	959	GGAGGACTGTCACCGGAGAGGACATGTGTACAGGGACTTGAAGCCCGAGAACTTGTCT	1018	
Qy	972	GGATGACTTGGGCAACTGCAAGTTATCTGACTTGGGGCTGTGCGTGTGAGATGAAAGGATG	1031	
Db	1019	GGATGACACAGGCGCACATCGCATCTCTGAACCTGGAGCTAGAGTGTGCAATGTGCCAG	1078	
Qy	1032	CAGCCATTCACCGAGAGGGCTGAAACAAATGTTACATGGCTCTTGAGATCTTAATGA	1091	

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QY 1272 AGATATTTCAGAGCTCTTTTGGCTTAAGAAACGAGCAACGCTTAGAACCAAGAAAA 1331

Db 1316 ACTTGCTACAGCTCCTCTGCAAGGACCTGCGGAACGCTGGGGGTGTGTTGGGGCGAG 1375

QY 1332 GTCTGATGATCCCAAGAAACATCATTTCTTTAAACATCAATCTTCTCGCTCGAAGC 1391

Db 1376 TGCCCCGAGGTGAAGAGACCCCTCTTTAAGAACTGAATTTCAAGCGGCTGGAGC 1435

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Db 1436 TGGCATCTGAGAGCCGCGCTTCAAGCCTGACCCCGACCATTTATCTGCAAGATGTCT 1495

QY 1452 TGAAATTGATGATTTCTCTGAGCTTGGGGGGTGGAAATTGATGACAAAGATAGCAGTT 1511

Db 1496 GGAATTTGAACAGTCTCTACGCTCAAGGAGCGTGAAGCTGAGCTACGACCGACGACTT 1555

QY 1512 CTTCAAAACTTTGGCAGACAGTGTCTGTCTTATAGCATGCGAGAGAAATTAAGAAAC 1571

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QY 1572 GGGACTGTTTGAAGAACTGAATGAC 1596

Db 1616 CGAGTGTCTCAAGAGCTGAATGTC 1640

RESULT 15

US-10-159-856-4

/ Sequence 4, Application US/10159856

/ Publication No. US20030228689A1

/ GENERAL INFORMATION:

/ APPLICANT: Susan M. Freier

/ APPLICANT: Kenneth W. Dobie

/ TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION

/ FILE REFERENCE: RTS-0365

/ CURRENT APPLICATION NUMBER: US/10/159, 856

/ CURRENT FILING DATE: 2002-05-31

/ NUMBER OF SEQ ID NOS: 134

/ SEQ ID NO 4

/ LENGTH: 2848

/ TYPE: DNA

/ ORGANISM: H. sapiens

/ FEATURE:

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (63)...(1793)

US-10-159-856-4

Query Match 25.2%; Score 418.2; DB 16; Length 2848;

Best Local Similarity 56.2%; Pred. No. 1,1e-117;

Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

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Db 65 GAGGCTTCGGAACATCGTACGGAACAGGTCTACTCAAGAGCCCGGAGAGAGTGGCGGTGG 124

QY 75 CGACAGCAAG--AGCTGCAAGCGGCGGCGGTAGGCTTGAGCTTCCCGGGCTGACAGG 131

Db 125 AATTCGAAAGCAAAAGCAAGAAATGGGGGAGATGCTCAGATTCTTCACATCAACCA 184

QY 132 CTGGCGAGAGCTCCGCGAAGCTGTCCTGAACTTCCACAGCCTGTGTAGACAGAGCC 191
 Db 185 GTGGAGAGAGCTGCGCTCAAGCTCAAGCGTGAATACAGAGCTGTGCGAGCGCAGC 244
 QY 192 CATGGATCGCGCGCTCTTCTCGTGAATCTTCTAGCAGAGTCCCAAGCCCTTCCCGAGGCGC 251
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 QY 252 AACCTTCTAGAGAGCTGCGAAGCTGCGAGAGCTGCGAGAGAGAGCCACCAAGAGAG 311
 Db 305 CGCTTCTCTGAGATGGGGGTGGCCAGTATGAAATGACCCCGAGAGAGAGAGAGAG 364
 QY 312 CGGCTGAGAGAGAGCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
 Db 365 TGGAG 421
 QY 372 CTTCCTCAGCAG 431
 Db 422 GGTCCCGCGAG 480
 QY 432 GGTGCGAGTGAAGCTGCGCGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
 Db 481 ACCCTTTCAG 538
 QY 492 GGAATTCGAG 551
 Db 539 CGACTTCTCAG 598
 QY 552 ACCAGTGTGAG 611
 Db 599 GCCAGTGAACAG 658
 QY 612 GGTATGTCCTGCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
 Db 659 GGTGTCCTGCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
 QY 672 GAAGCGCTGAAG 731
 Db 719 AAAGCGATCAAG 778
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 Db 779 GAAGGTGAAG 838
 QY 792 CTGCTTGTCAAG 851
 Db 839 GTGCTGTGTGAG 898
 QY 852 GAGCGTGTGTGAG 911
 Db 899 CAGGCTGTGTGAG 958
 QY 912 GCTGACCTCAATGAAG 971
 Db 959 GAG 1018
 QY 972 GATGAG 1031
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 QY 1032 CAAGCGATCAAG 1091
 Db 1079 CAAGCGATCAAG 1135
 QY 1092 AAAGGTGAAG 1151
 Db 1136 GAATGAG 1195
 QY 1152 GGTGCTGAG 1211
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QY 1212 GCAAG 1271
 Db 1256 GCGGCTGTGAG 1315
 QY 1272 AATATTTGAG 1331
 Db 1316 ACTTGTGTCAAG 1375
 QY 1332 GTCTGATATTCAG 1391
 Db 1376 TGCCGCGAG 1435
 QY 1392 TGAGCTATGAG 1451
 Db 1436 TGAGCTATGAG 1495
 QY 1452 TGAGCTATGAG 1511
 Db 1496 GAGACTTGAAG 1555
 QY 1512 CTGAG 1571
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 QY 1572 GAGACTGTGAG 1596
 Db 1616 GAGACTGTGAG 1640

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 Job time : 527.034 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 10:30:45 ; Search time 4319.34 Seconds

(without alignments)
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Title: US-10-044-205a-3

Perfect score: 1659

Sequence: 1 atgtgtgacatgggggacct.....ctggcgtgtgtttgtatgt 1659

Scoring table: IDENTITY NTC

Gapop 10.0, Gapept 1.0

Searched: 3470272 seqs, 21671516935 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
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40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1659	100.0	1659	6	AX797554
2	1659	100.0	2198	6	AX797552
3	1655.8	99.8	1662	6	AX64368
4	1655.8	99.8	1761	6	BD186115
5	1655.8	99.8	1799	9	AF439409
6	1655.8	99.8	2249	6	AR225819
7	1655.8	99.8	2249	6	AX252443
8	1655.8	99.8	3186	6	AX170216
9	1655.8	99.8	3186	6	AF282269
10	1655.4	99.8	1662	6	AR225817
11	1654.2	99.8	1662	6	AX252439
12	1654.2	99.7	1662	6	AR263766
13	1654.2	99.7	1662	6	AR343544
14	1654.2	99.7	1662	6	AX357902
15	1652.6	99.6	1662	6	AX166511
16	1652.6	99.6	1662	6	AX170213
17	1589.8	95.8	1701	6	AX921933
18	1299.8	78.3	2453	4	AF282270
19	1294.8	78.0	2420	4	AF049726
20	1208.6	72.9	3095	10	AF063016
21	1187.8	71.6	1191	6	BD186106
22	1046.8	63.1	1062	6	AR225818
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24	617.4	37.2	36651	6	AR263767
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26	617.4	37.2	36651	6	AX357904
27	617.4	37.2	125041	2	AC068693
28	571.8	34.5	215077	5	AC112504
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31	424.6	25.6	2105	9	BC017272
32	423.8	25.5	2898	4	BOVHRK1N
33	423	25.5	1789	9	AF040752
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35	423	25.5	2708	9	BC009277
36	419.8	25.3	2848	6	AR160365
37	418.8	25.2	2549	9	U00686
38	418.2	25.2	2204	6	I23378
39	418.2	25.2	2204	6	I33280
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41	418.2	25.2	2848	9	HUMPROCKT
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43	408.6	24.6	1806	10	MM15799
44	408.6	24.6	1858	10	MM15797
45	408.6	24.6	1952	10	AF040749

ALIGNMENTS

RESULT 1
AX797554
LOCUS AX797554
DEFINITION Sequence 3 from Patent WO02095032.
ACCESSION AX797554
VERSION AX797554.1 GI:37518056
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Kapeller-Ribermann, R. and Bandaru, R.
TITLE Method and compositions of human proteins and uses thereof
JOURNAL Patent: WO 02095032-A 3 28-Nov-2002;

ORIGIN

/note="Incyle ID No: 7477204CBI"

Query Match 99.8%; Score 1655.8; DB 6; Length 1662;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
 BD186115 1761 bp DNA linear PAT 17-JUN-2003
 LOCUS A novel gene relating to disease and use thereof.
 DEFINITION BD186115
 ACCESSION BD186115.1 GI:31878315
 VERSION WO 02103020-A/10.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eularchia; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1761)
 Koyama, N., Tanida, S., and Yamamoto, K.
 A novel gene relating to disease and use thereof
 Patent: WO 02103020-A 10 27-DEC-2002;
 TAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI
 YAMAMOTO
 OS Homo sapiens (human)
 PN WO 02103020-A/10
 PD 27-DEC-2002
 PF 14-JUN-2002 WO 2002P005942
 PR 15-JUN-2001 JP OIP 182654
 PI NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO
 PC C12N15/54, C12N9/12, G01N33/50, G01N33/15, C07K16/40, A61K39/395 CC
 A novel gene relating to disease and use thereof FH Key
 Location/Qualifiers

FT source 1..1761
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ORIGIN

Query Match 99.8%; Score 1655.8; DB 6; Length 1761;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGACATGGGGGCTTGGACAACTGATGCAACCGCTTACCTGACGCCCCG 60
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RESULT 5
 AF439409 1799 bp mRNA linear PRI 21-FEB-2002
 LOCUS
 DEFINITION Homo sapiens G-protein-coupled receptor kinase 7 (GRK7) mRNA,
 AK7-S allele, complete cds.
 ACCESSION AF439409
 VERSION AF439409.1 GI:17933258
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1799)
 Chen, C.K., Zhang, K., Church-Kopple, J., Huang, W., Zhang, H.,
 Chen, Y.J., Frederick, J.M., and Baehr, W.
 Characterization of human GRK7 as a potential cone opsin kinase
 MOL. VIS. 7, 305-313 (2001)
 JOURNAL MEDLINE 21626361
 PUBMED 11754336
 REFERENCE 2 (bases 1 to 1799)

AUTHORS Baehr, W. and Chen, C.-K.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15 North/2030 East, Salt Lake City, UT 84112, USA

FEATURES
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gene
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ORIGIN
 Query Match 99.8%; Score 1655.8; DB 9; Length 1799;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 ATGGTGAACATGGGGGCTCTGACAACTGATCGCAACCGCTTACTGACAGCCCGG 60
 138 ATGGTGAACATGGGGGCTCTGACAACTGATCGCAACCGCTTACTGACAGCCCGG 197
 61 AAGCCCTCGGACTGACAGCAAGAGCTGACAGGCGGCGGCTGAGCCCTGCGCC 120
 198 AAGCCCTCGGACTGACAGCAAGAGCTGACAGGCGGCGGCTGAGCCCTGCGCC 257
 121 GGGCTGAGGCTGACAGCAAGAGCTGACAGGCGGCGGCTGAGCCCTGCGCC 180
 258 GGGCTGAGGCTGACAGCAAGAGCTGACAGGCGGCGGCTGAGCCCTGCGCC 317
 181 GAGCAGAGCCCATGCTGCGCGCTCTCTCTGACCTTCTTACCCACAGTCCCAAGCTTC 240
 318 GAGCAGAGCCCATGCTGCGCGCTCTCTCTGACCTTCTTACCCACAGTCCCAAGCTTC 377
 241 CGCAAGCGGCAACCTTCTTACAGAGAGCTGACAGGCGGCGGCTGAGCCCTGCGCC 300
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 301 ACCAAGAGAGCGGCTGACAGGAGCTGAGCACTTGTGAGTCCCTTGTCCCGGGG 360
 438 ACCAAGAGAGCGGCTGACAGGAGCTGAGCACTTGTGAGTCCCTTGTCCCGGGG 497
 361 AACCCGCAACCTTCTTCTGACAGGCGGCTTCTTACAGCAAGTTCGAGGAACTC 420
 498 AACCCGCAACCTTCTTCTGACAGGCGGCTTCTTACAGCAAGTTCGAGGAACTC 557
 421 GAAAGGAGAGTGGCTGAGTACGCTGCAAGGCTGAGGCACTGAGCTTCTTGAAGAG 480
 558 GAAAGGAGAGTGGCTGAGTACGCTGCAAGGCTGAGGCACTGAGCTTCTTGAAGAG 617
 481 GAGCCCTTTAAGATTTCTGACAGGCGCTTCTTACAGCAAGTTCGAGGAACTC 540
 618 GAGCCCTTTAAGATTTCTGACAGGCGCTTCTTACAGCAAGTTCGAGGAACTC 677

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Query Match 99.8%; Score 1655.8; DB 9; Length 1799;
 Best Local Similarity 99.9%; Pred. No. 0;
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 498 AACCCGCAACCTTCTTCTGACAGGCGGCTTCTTACAGCAAGTTCGAGGAACTC 557
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 558 GAAAGGAGAGTGGCTGAGTACGCTGCAAGGCTGAGGCACTGAGCTTCTTGAAGAG 617
 481 GAGCCCTTTAAGATTTCTGACAGGCGCTTCTTACAGCAAGTTCGAGGAACTC 540
 618 GAGCCCTTTAAGATTTCTGACAGGCGCTTCTTACAGCAAGTTCGAGGAACTC 677

QY 541 TTGAGATGCAACCAAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGT 600
 DB 678 TTGAGATGCAACCAAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGT 737
 QY 601 GGTGTTGGGAGGTAATGTGCGCTGACAGGTGAAAACCACTGGGAAAGTATGACCTGAAG 660
 DB 738 GGTGTTGGGAGGTAATGTGCGCTGACAGGTGAAAACCACTGGGAAAGTATGACCTGAAG 797
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 QY 1261 GAG 1320
 DB 1398 GAG 1457
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 QY 1441 AAG 1500
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RESULT 6
LOCUS AR225819 2249 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6444456.
ACCESSION AR225819
VERSION AR225819.1 GI:27263949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2249)
AUTHORS Walke,D.W., Wilgenowski,N.I. and Turner,C.A. Jr.
TITLE Human G-coupled protein receptor kinases and polynucleotides
JOURNAL Patent: US 644456-A 5 03-SEP-2002;
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Query Match 99.8%; Score 1655.8; DB 6; Length 2249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGAATGATGGGGGCTTGGACAACTGATGCGCAACAGCGGCTTCTGGAGGCGG 60
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QY 61 AAGCCCTGCGATCTGCGACAGCAAGAGCTGAGGCGGCGGCTGAGCCTGCGCC 120
Db 414 AAGCCCTGCGATCTGCGACAGCAAGAGCTGAGGCGGCGGCTGAGCCTGCGCC 473
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RESULT 7
LOCUS AX252443 2249 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 5 from Patent WO0168869.

ACCESSION AX252443
VERSION AX252443.1 GI:15985735
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Walke,D.W., Wilganowski,N.L. and Turner,C.A.
TITLE Human g-coupled protein receptor kinases and polynucleotides
JOURNAL Patent: NO 0168869-A 5 20-SEP-2001;
Lexicon Genetics Incorporated (US)
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Best Local Similarity 99.9%; Pred. No. 0;
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QY 841 TACAGTGTGAG 900
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QY 901 GCTGTGAG 960
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DB 1374 ATGAG 1433
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QY 1141 ATTATTAATGAG 1200
DB 1494 ATTATTAATGAG 1553
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DB 1554 GAGAGTGTGAG 1613
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QY 1381 GCGCTGAG 1440
DB 1734 GCGCTGAG 1793
QY 1441 AAGAGATGCTGAG 1500
DB 1794 AAGAGATGCTGAG 1853
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DB 1854 GATTAAG 1913
QY 1561 ATTATTAAG 1620
DB 1914 ATTATTAAG 1973
QY 1621 GAGGATTAATTCAG 1680
DB 1974 GAGGATTAATTCAG 2037
RESULT 8
AX710216 3186 bp DNA linear PART 10-APR-2003
LOCUS AX710216
DEFINITION Sequence 4 from Patent WO03018815.
ACCESSION AX710216
VERSION AX710216.1 GI:29786804
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Xiao, Y.
TITLE Regulation of human g protein-coupled receptor kinase
JOURNAL Patent: WO 03018815-A 4 06-MAR-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
Source 1.3186
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.8%; Score 1655.8; DB 6; Length 3186;
Best Local Similarity 99.94; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGATGACATGGGGGCGCTGGACAACTGATCCGCAACCGGCTTACCTGGACGGCCGG 60
85 ATGATGACATGGGGGCGCTGGACAACTGATCCGCAACCGGCTTACCTGGACGGCCGG 144
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121 GGGCTGACAGGGGCTGGGAGAGCTGCGCCAGAGCTGCTCCCTGAATTCCAGAGCTG 180
205 GGGCTGACAGGGGCTGGGAGAGCTGCGCCAGAGCTGCTCCCTGAATTCCAGAGCTG 264
181 GAGCAGCAGCCCATCGTCCGCGCTTCCGTAATCTTCCGCAAGTCCCAAGTTC 240
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241 CGCAAGCGGCAACCTTCTTAAGAGAGCTGAGCACTGGAGTCCGCAAGAGAGAGCC 300
325 CGCAAGCGGCAACCTTCTTAAGAGAGCTGAGCACTGGAGTCCGCAAGAGAGAGCC 384
301 ACCAAGACACCGGCTGAGAGGGGCTGTGGCCATTGTGCGAGTCCCTGCGCGG 360
385 ACCAAGACACCGGCTGAGAGGGGCTGTGGCCATTGTGCGAGTCCCTGCGCGG 444
361 AACCCGCAACCTTCTTCCAGCGGCGGCTGCGCCCAAGTCCGCAAGAGAGAGAG 420
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421 GAAAGCGAGTGTGCTGAGTGAAGCTGCGCAAGCTGAGCGCATGCTTCTTGGAGAG 480
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625 TTGAGATGCAACAGTGTGAGACAGTACTTACAGAGTTCAAGAGTCCGAGGAGAGT 684
601 GGTTTGGAGAGGTATGTGCGTCCAGTGAAGAAACCTGGAGAGAGTATGCTGTAG 660
685 GGTTTGGAGAGGTATGTGCGTCCAGTGAAGAAACCTGGAGAGAGTATGCTGTAG 744
661 AAACCTGCAAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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1141 ATTTATGAATGCTGCTGAGCAACATTCATCAAGATTAACAAGAAAGGTCAATATA 1200
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1285 GAGGATCTGAAGCAAGAACTGCAAGAGAGAGTCAATTCAGAGATGATTAATCTTACA 1344
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1705 GAGGTAATTAATCAAGTCTGAGCTGTTGTTGTTATG 1743

RESULT 9

AP282269 3186 bp mRNA linear PRI 21-NOV-2001
LOCUS Homo sapiens g protein-coupled receptor kinase 7 mRNA, complete cds.

ACCESSION

AP282269
VERSION AP282269.1 GI:17026317

KEYWORDS

ORGANISM Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 3186)
Weiss, R.R., Dreesch, M.H., Horner, T.J., Li, A., Craft, C.M. and Osawa, S.

TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction

JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)

MEDLINE 21574315

PubMed 11717351

REFERENCE 2 (bases 1 to 3186)

AUTHORS Osawa, S. and Weiss, E.R.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

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/tissue_type="retina"

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ORIGIN

Query Match 99.8%; Score 1655.8; DB 9; Length 3186;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGTGTGACATGAGGGGGCCCTGACCAACCTGATGCGCAACGCGCTTACCTGAGGCGCGG 60
Db ATGTGTGACATGAGGGGGCCCTGACCAACCTGATGCGCAACGCGCTTACCTGAGGCGCGG 144
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Db 121 GGGCTGCAAGGCTGCGGAGCTCGCGCAAGAGCTGTCCTGAACTTCAACAGCTGTGT 264
Qy 205 GGGCTGCAAGGCTGCGGAGCTCGCGCAAGAGCTGTCCTGAACTTCAACAGCTGTGT 264
Db 181 GAGGAGAGCCCATGAGTGCAGCTCTTCTGCTGATCTTCTTACCAAGTCCCAAGCTTC 240
Qy 181 GAGGAGAGCCCATGAGTGCAGCTCTTCTGCTGATCTTCTTACCAAGTCCCAAGCTTC 240
Db 265 GAGGAGAGCCCATGAGTGCAGCTCTTCTGCTGATCTTCTTACCAAGTCCCAAGCTTC 324
Qy 241 CGCAAGCGGCAACCTTCTTGAAGAGCTGCAAGAGCTGGAAGTGGCGGAGAGAGAGAGCC 300
Db 325 CGCAAGCGGCAACCTTCTTGAAGAGCTGCAAGAGCTGGAAGTGGCGGAGAGAGAGAGCC 384
Qy 301 ACCAAGAGAGAGCGGCTGCAAGGCGCTGAGTGCACCTTGTGAGTGCAGCTTGTGCGGAG 360
Db 385 ACCAAGAGAGAGCGGCTGCAAGGCGCTGAGTGCACCTTGTGAGTGCAGCTTGTGCGGAG 444
Qy 361 AAGCCGCAACCTTCTTCAAGAGAGCTGAGTGCACCAAGTGCAGAGCCCAAGCTTGAAG 420
Db 445 AAGCCGCAACCTTCTTCAAGAGAGCTGAGTGCACCAAGTGCAGAGCCCAAGCTTGAAG 504
Qy 421 GAAAGAGAGAGTGTGAGTGCAGTGCAGAGCTGCAAGAGCTGAGTGCAGTGTCTTCTGAGAG 480
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Db 565 CAGCCCTTAAAGATTGTGAGTGCAGAGCTTCTTGAAGAGTTCGTGAGTGCAGAACTC 624
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Db 625 TTGAGATGCAACAGTGTGACAGAGTACTTCACTGAGTTCAGAGTGTGGGAGAGGT 684
Qy 601 GGTTTGGGAGAGTATGTGCGGCTGAGTGAAGAACTGAGAGATGATGCTGTGAAG 660
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Qy 661 AAACGTGACAGAGAGCGGCTGAGAGAGAGTGGCGAGAGAGTGGCTTCTTGGAGAG 720
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Db 865 AAGACCATCTGCTGCTTGTGATGAGCTGATGAGATGAGAGAGAGCTCAAGTTCACATC 924
Qy 841 TACAAGTGGGCAAGCTGTGCTGAGCATGAGCGGCTGATCTTTTACCTGGCCAGATA 900
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Db 1285 GAGGATGAG 1344
Qy 1261 GAGGAG 1320
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Qy 1321 AGCAG 1380
Db 1405 AGCAG 1464
Qy 1381 CGCTGAG 1440
Db 1465 CGCTGAG 1524
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Db 1525 AAGAGCATGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1584
Qy 1501 GATTAAG 1560
Db 1585 GATTAAG 1644
Qy 1561 ATTATGAAG 1620

Db 1645 ATTATGAAACGGGACTGTTTGAAGACTGATGACCCCAAGACCTTACGGTTTGAG 1704
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Db 1705 GAGGTATTCATCCAAAGTCGGCTGTGTTTGTATTG 1743

RESULT 10
AR225817 1662 bp DNA linear PAT 20-DEC-2002
LOCUS AR225817
DEFINITION Sequence 1 from patent US 6444456.
ACCESSION AR225817
VERSION AR225817.1 GI:27263947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
TITLE Human G-coupled protein receptor kinases and polynucleotides
encoding the same
JOURNAL Patent: US 6444456-A 1 03-SEP-2002;
FEATURES
Location/Qualifiers
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source /organism="Unknown"
/mol_type="genomic DNA"

Query Match 99.8%; Score 1655.4; DB 6; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 GGGCTGCAAGGCTGCGAGAGCTGCGAGAGAGCTGCGTGAAGCTTCCAGCAAGCTGCTGT 180
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Qy 181 GAGCAGACGCCATCGGTGCGGCTCTTCCGTGACTTCTTACGCAAGTCCAGCTTC 240
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Db 241 CGCAAGGCGCAACCTTCCAGAGAGAGCTGCAAGAGCTGAGAGCTGCGCGAGAGAGCC 300
Qy 301 ACCAAAGACAGCGAGCTGAGAGGAGCTGAGGAGCACTTGTGAGAGTGCCTGCGCGGG 360
Db 301 ACCAAAGACAGCGAGCTGAGAGGAGCTGAGGAGCACTTGTGAGAGTGCCTGCGCGGG 360
Qy 361 AACCCGCAACCTTCTTCAAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAG 420
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Query Match	99.7%	Score 1654.2;	DB 6;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1656; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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Dp	841	TACAACTGGGAGACGCGCTGGCTCGGACATGAGCCGGAGTATCTTTTACTCGGCCAGATA	900
Qy	901	GCTGTGGGAGTCTGACACCTCCATGTAACCTGGGATCGTCTATTCGGGACATGAACTCGAG	960
Dp	901	GCTGTGGGAGTCTGACACCTCCATGTAACCTGGGATCGGATCGTCTATTCGGGACATGAACTCGAG	960
Qy	961	AATGTGCTTCTGATGACCTTCGGCAATCGAGGTTATCTGACCTGGGGGTGGCGGTGGAG	1020
Dp	961	AATGTGCTTCTGATGACCTTCGGCAATCGAGGTTATCTGACCTGGGGGTGGCGGTGGAG	1020
Qy	1021	ATGAAAGGTGGAGAACCCCATCACTCGAAGGGCTGGAAACAAATGTTTAACTGACCTCTGAG	1080
Dp	1021	ATGAAAGGTGGAGAACCCCATCACTCGAAGGGCTGGAAACAAATGTTTAACTGACCTCTGAG	1080
Qy	1081	ATCCCAATGAAAAAGATGATATCCCTATCCCTGGTGGACATGGTTGGCCATGGGATGCAAC	1140
Dp	1081	ATCCCAATGAAAAAGATGATATCCCTATCCCTGGTGGACATGGTTGGCCATGGGATGCAAC	1140
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Dp	1141	ATTATGAAATGTGTGCTGGAGAACCACTTCAAAAGATTAACAGGAAAAAGTCACTAA	1200
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Dp	1201	GAGGATCTGAAGCAAAAGATCTCTGGAGAGAGAGGTCAAAATTCAGCATGATAACTTACA	1260
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Dp	1261	GAGGAAGCAAAAGATATTGTTCAGAGCTCTTCTTGCTGTAGAAACAGAGCAACGCTTAGGA	1320
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Dp	1381	CGCCTGAAAGCTGGCCCAATTGGAACCCCCATTGTGGCAACACCTTCAGTGGTTATGCG	1440
Qy	1441	AAAGACATCGCTGAAATATGATGATTTCTCTGAGGTTGGGGGGGTGGAATTTGATGACAA	1500
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Dp	1501	GATPAGCAAGTCTTTCAAAACTTTGGGCAAGGTGTCTTCTATATGCAATGGCAGGAAGAA	1560
Qy	1561	ATTATAGAAACGGGACCTGTTTGAAGAACTGATGACCCCAAGACCTTACGGGTTTGTAG	1620
Dp	1561	ATTATAGAAACGGGACCTGTTTGAAGAACTGATGACCCCAAGACCTTACGGGTTTGTAG	1620
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Dp	1621	GAGGTAATTCATCCCAAGTCTGGCGGTGTGTTGTTATG	1659
RESULT 13			
LOCUS AR343544			
DEFINITION Sequence 1 from patent US 6579709.			
ACCESSION AR343544			
VERSION AR343544.1 GI:33739257			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
REFERENCE 1 (bases 1 to 1662)			
AUTHORS Gueglier, K., Beasley, E. M. and Di Francesco, V.			
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof			

Query Match	99.7%	Score 1654.2;	DB 6;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1656; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	1	AATGGTGAACATGGGAGGCGCTTGAGCAACCTGATGGCCAAACCGGCTTACCTGAGAGCCGG	60
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QY	61	AAGCCCTCGAGCTGGAGCAGCAAAAGAGCTGAGAGGAGGCGCGGCTAGCTGGCCCTTGGCC	120
Db	61	AAGCCCTCGAGCTGGAGCAGCAAAAGAGCTGAGAGGAGGCGCGGCTAGCTGGCCCTTGGCC	120
QY	121	GGGCTGCAAGGAGCTGGCGGAGCTCGAGCAGAAAGCTGTCCCTGAATCTTCCACAGGCTGTGT	180
Db	121	GGGCTGCAAGGAGCTGGCGGAGCTCGAGCAGAAAGCTGTCCCTGAATCTTCCACAGGCTGTGT	180
QY	181	GAGGAGAGAGCCCATAGGTGGTGGCCGCTCTTTCCGTGACCTTCCTAGACAGTGGCCACGTTT	240
Db	181	GAGGAGAGAGCCCATAGGTGGTGGCCGCTCTTTCCGTGACCTTCCTAGACAGTGGCCACGTTT	240
QY	241	CGCAAGCGGCAACCTTCTCTAGAGACCTGACAACTGGAGAGCTGGCGGAGAGAGAGACCC	300
Db	241	CGCAAGCGGCAACCTTCTCTAGAGACCTGACAACTGGAGAGCTGGCGGAGAGAGAGACCC	300
QY	301	ACCAAAACAGAGCGGCGCTTGCAAGGAGCTGGTGGCACTTGTGCAAGTGGCCCTTGGCGGAG	360
Db	301	ACCAAAACAGAGCGGCGCTTGCAAGGAGCTGGTGGCACTTGTGCAAGTGGCCCTTGGCGGAG	360
QY	361	AACCGCAACCTTTCTCTCAACCCAGAGCGGTGGGCAACCAAGTGGCAACAGCCACACTGAG	420
Db	361	AACCGCAACCTTTCTCTCAACCCAGAGCGGTGGGCAACCAAGTGGCAACAGCCACACTGAG	420
QY	421	GAAAGAGCAGTGGCTGACAGTGAACGCTGGGCAAGAGCTGAGGCACTGGCTTTCTTGGCAAG	480
Db	421	GAAAGAGCAGTGGCTGACAGTGAACGCTGGGCAAGAGCTGAGGCACTGGCTTTCTTGGCAAG	480
QY	481	CAGGCTCTTAAAGATTTTCGTGACAGAGGCTTTCTACAGCAAGTTTCTGCAGTGGAAACTC	540
Db	481	CAGGCTCTTAAAGATTTTCGTGACAGAGGCTTTCTACAGCAAGTTTCTGCAGTGGAAACTC	540
QY	541	TTGAGATGCAACAGAGTGCACAGCAAGATCTTCACTAGAGTTCCAGAGTGGGAGAAAGGT	600
Db	541	TTGAGATGCAACAGAGTGCACAGCAAGATCTTCACTAGAGTTCCAGAGTGGGAGAAAGGT	600
QY	601	GGTTTGGGAGAGTATGTGCGCTTCAGGTGAAAAACACTGGAGAGATATGCTGTAG	660
Db	601	GGTTTGGGAGAGTATGTGCGCTTCAGGTGAAAAACACTGGAGAGATATGCTGTAG	660
QY	661	AAACTGACAAAGAGCGGCTGAAAGAAAGAGTGGCGGAGAAATGGCTCTTTGGAAAAG	720
Db	661	AAACTGACAAAGAGCGGCTGAAAGAAAGAGTGGCGGAGAAATGGCTCTTTGGAAAAG	720
QY	721	GAAATCTTGGAGAGGTGACAGGCCCTTTCATTTGTCTCTGTGGCGCTATGCTTTGAGAGC	780
Db	721	GAAATCTTGGAGAGGTGACAGGCCCTTTCATTTGTCTCTGTGGCGCTATGCTTTGAGAGC	780
QY	781	AAGACCCATCTCTGCTTGTCTATGAGCTGTGATGGGAGAGACCTTCAAGTTCCATCTC	840
Db	781	AAGACCCATCTCTGCTTGTCTATGAGCTGTGATGGGAGAGACCTTCAAGTTCCATCTC	840
QY	841	TACACAGTGGGCAACGGTGGCTTGAGACATGAGACCTGGGAGATCTTTTATCTGGGCCCAATA	900
Db	841	TACACAGTGGGCAACGGTGGCTTGAGACATGAGACCTGGGAGATCTTTTATCTGGGCCCAATA	900
QY	901	GCTTGGGAGATGCTGACCTTCATGAACTTGGCAATGCTTATCTGGGACATGAGCTTGA	960
Db	901	GCTTGGGAGATGCTGACCTTCATGAACTTGGCAATGCTTATCTGGGACATGAGCTTGA	960
QY	961	AATGTGCTTGTGATGACCTGGGCAATGAGAGTTATCTGACCTGGGAGCTGGCGGAG	1020
Db	961	AATGTGCTTGTGATGACCTGGGCAATGAGAGTTATCTGACCTGGGAGCTGGCGGAG	1020

QY	1021	ATGAAAGGAGCGAAGCCCATACCCAGAGGGCTGGAAACATATGGTTACATAGCTCTCCGAG	1080
Db	1021	ATGAAAGGAGCGAAGCCCATACCCAGAGGGCTGGAAACATATGGTTACATAGCTCTCCGAG	1080
QY	1081	ATCTCATATGAAAAAGTAAGTTATCTCATCTGTGSACTGGTTTGCATGGAGATGCAG	1140
Db	1081	ATCTCATATGAAAAAGTAAGTTATCTCATCTGTGSACTGGTTTGCATGGAGATGCAG	1140
QY	1141	ATTATAGAAATGCTGTGTGGAGAAACACATTCGAAAGTTACAGGAAAGGTCAGTAA	1200
Db	1141	ATTATAGAAATGCTGTGTGGAGAAACACATTCGAAAGTTACAGGAAAGGTCAGTAA	1200
QY	1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGAGAGGTCAATTCGACATGATATCTTCACA	1260
Db	1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGAGGTCAATTCGACATGATATCTTCACA	1260
QY	1261	GAGAGAGCAAAAGATATTTGACAGGCTCTTCTGAGTCAGAAACAGAGCAAGCTTAGGA	1320
Db	1261	GAGAGAGCAAAAGATATTTGACAGGCTCTTCTGAGTCAGAAACAGAGCAAGCTTAGGA	1320
QY	1321	AGCAGAGAAAAGTCGTAGATATCCAGGAAACATCTTCTTTAAACATATCACTTCTCT	1380
Db	1321	AGCAGAGAAAAGTCGTAGATATCCAGGAAACATCTTCTTTAAACATATCACTTCTCT	1380
QY	1381	CGCTGAGAGCTGGCTTAATTGAAACCCCTTTGTGTGCAGACCTTCAGTGGTTATATGC	1440
Db	1381	CGCTGAGAGCTGGCTTAATTGAAACCCCTTTGTGTGCAGACCTTCAGTGGTTATATGC	1440
QY	1441	AAAGGACATCGCTGAATATGATATTTCTCTGAGGTTGAGGGGAGTGAATTTGATGACAA	1500
Db	1441	AAAGGACATCGCTGAATATGATATTTCTCTGAGGTTGAGGGGAGTGAATTTGATGACAA	1500
QY	1501	GATAGACAGTCTTCTCAAAAACCTTTGCGACAGGTGTGTGTCCTATAGCATATGCGAGAA	1560
Db	1501	GATAGACAGTCTTCTCAAAAACCTTTGCGACAGGTGTGTGTCCTATAGCATATGCGAGAA	1560
QY	1561	ATTATAGAAACGAGACTGTTTGAAGACTGATATGCCCAAGACACTTACGGGTTGTGAG	1620
Db	1561	ATTATAGAAACGAGACTGTTTGAAGACTGATATGCCCAAGACACTTACGGGTTGTGAG	1620
QY	1621	GAGGGTATTCATCAACAGCTCGAGGTGTGTGTTATATG	1659
Db	1621	GAGGGTATTCATCAACAGCTCGAGGTGTGTGTTATATG	1659

Query Match	99.6%	Score 1652.6;	DB 6;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1655; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Plotman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S.	Novel human protein kinases and protein kinase-like enzymes	Patent: WO 0138503-A 2 31-MAY-2001;	Location/Qualifiers 1..1662
		/organism="Homo sapiens"		
		/mol_type="unassigned DNA"		
		/db_xref="taxon:9606"		

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: August 13, 2004, 06:21:35 ; Search time 444.751 Seconds

(without alignments)
15846.518 Million cell updates/sec

Title: US-10-044-205A-3

Perfect score: 1659
Sequence: 1 atgtgtgacatgaggggccccct.....ctggcgtgtgttttattatg 1659

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq 29Jan04:*
2: geneseq1980s:*
3: geneseq1990s:*
4: geneseq2000s:*
5: geneseq2001s:*
6: geneseq2002s:*
7: geneseq2003s:*
8: geneseq2003bs:*
9: geneseq2003cs:*
10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1659	100.0	2198	7	ABSS57375
2	1655.8	99.8	1662	6	ABQ86178 Novel hum
3	1655.8	99.8	1662	6	AD26466 Human kin
4	1655.8	99.8	1662	6	AD46350 Human con
5	1655.8	99.8	1761	7	AB256943 Human gen
6	1655.8	99.8	1821	9	AD339221 Novel hum
7	1655.8	99.8	2249	4	AAH78799 Human G-P
8	1655.8	99.8	3186	7	ACC44827 Human G-P
9	1654.2	99.7	1662	4	AAH78797 Human G-P
10	1654.2	99.7	1662	6	AD28071 Human kin
11	1652.6	99.6	1662	4	AA506702 Human kin
12	1652.6	99.6	1662	7	ACC44826 Human G-P
13	1187.8	71.6	1191	7	AB256934 Human RGS
14	1094.2	66.0	1486	6	AAH46351 Human con
15	1046.8	63.1	1062	6	AAH78798 Human G-P
16	617.4	37.2	36651	6	AAH24842 Human kin
17	419.8	25.3	2848	4	AAH24842 Human kin
18	418.2	25.2	2204	2	AAH24842 Human kin
19	418.2	25.2	2848	6	AB161805 Human GRK
20	418.2	25.2	2848	6	AB161805 Human GRK
21	403.8	24.3	2541	9	AD553307 CDNA enco
22	395.8	23.9	1983	2	AAH78797 Rat GRK c
23	389.4	23.5	2206	2	AAH78797 Rat GRK c

24	377.8	22.8	2519	7	ACA03892	ACA03892 CDNA upre
25	374.6	22.6	2519	9	ADB47372	ADB47372 Human CDN
26	373	22.5	2511	2	AAV71032	AAV71032 GrK5-gree
27	373	22.5	2529	2	AAV71024	AAV71024 GrK5-gree
28	373	22.5	2557	6	AAH36142	AAH36142 Human G p
29	373	22.5	2557	7	ACA56700	ACA56700 Human sig
30	369	22.2	1996	5	AAH80696	AAH80696 DNA enco
31	368.2	22.2	2557	6	ABK49404	ABK49404 CDNA enco
32	366.6	22.1	2557	4	AAH24841	AAH24841 Nucleotid
33	327.2	19.7	3836	4	ABL19581	ABL19581 Drosophila
34	320.6	19.3	2017	2	AAH90219	AAH90219 GRK4 poly
35	320.6	19.3	2113	2	AAH90218	AAH90218 GRK4 poly
36	311.6	18.8	1879	2	AAH90221	AAH90221 GRK4 poly
37	311.6	18.8	1886	2	AAH90222	AAH90222 GRK4 poly
38	311.6	18.8	1975	2	AAH90220	AAH90220 GRK4 poly
39	262.4	15.8	2947	5	AAH86360	AAH86360 DNA enco
40	253.2	15.3	1324	2	AAH90223	AAH90223 GRK4 poly
41	246.8	14.9	1420	2	AAH90222	AAH90222 GRK4 poly
42	158.4	9.5	493	8	ACH50623	ACH50623 Human mam
43	153.4	9.2	3154	8	ACD44895	ACD44895 Human sig
44	151	9.1	2037	6	ABT06290	ABT06290 Human NOV
45	151	9.1	2067	6	AAK96675	AAK96675 2067nt hu

ALIGNMENTS

RESULT 1	ABSS57375	standard, CDNA, 2198 BP.
ID	ABSS57375	
AC	ABSS57375	
XX		
DT	04-FEB-2003	(first entry)
XX		
DE	CDNA encoding human GPCR kinase (GPCRK) 69087.	
XX		
KW	Human; G protein coupled receptor kinase; GPCR 69087;	
KM	cellular proliferative disorder; differentiative disorder;	
KW	haematopoietic neoplastic disorder; leukaemia; sarcoma;	
KW	metastatic disorder; cytostatic; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FM	Key	Location/Qualifiers
FT	CDS	291..1952
FT		/tag= a
FT		/product= "GPCRK 69087"
FT		/note= "The coding sequence given as SEQ ID No.3 is specifically claimed in Claim 1"
XX		
XX	US2002123464-A1.	
XX		
XX	05-SEP-2002.	
XX		
XX	22-OCT-2001; 2001US-00044205.	
XX		
PR	19-OCT-2000; 2000US-0241884P.	
PR	20-OCT-2000; 2000US-0241877P.	
PR	23-OCT-2000; 2000US-0242428P.	
XX		
XX	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Kapeller-Liebermann R, Bandaru R;	
DR	WPI: 2003-066811/06.	
DR	P-PSDB; ABG72173.	
XX		
XX	Novel isolated G protein coupled receptor kinase, 69087, nuclear	
PT	signaling protein, 15821 or mitogen activated protein kinase phosphatase,	
PT	15418, useful for treating cellular proliferative or differentiative	
PT	disorders.	
XX		

PS Claim 1, Fig 1; 98bp; English.

XX The present invention relates to the isolation of a novel human G protein coupled receptor (GPCR) kinase (GPCR) designated 69087, a novel human nuclear signalling protein designated 15821, and a novel human mitogen-activated protein kinase (MAPK) phosphatase MAPK designated 15418, and the polynucleotide sequences encoding them. The sequences of the CC invention are useful for treating and diagnosing disorders such as CC cellular proliferative and differentiative disorders (e.g. haematopoietic CC neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic CC disorders). They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive CC medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical CC trials and pharmacogenomics), and in methods of treatment (e.g. CC therapeutic and prophylactic). The sequences may also be used to screen CC public databases to identify other family members or related sequences. CC The polypeptide sequences are useful as immunogens to generate antibodies CC that bind the polypeptides. The polynucleotide sequences are useful for CC mapping their respective genes on a chromosome, identifying gene regions CC associated with cellular proliferative or differentiative disorders, and CC in gene therapy. The present sequence encodes human GPCR 69087.

XX Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

Query Match 100.0%; Score 1659; DB 7; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGACATGAGGAGCCCTGACAACTGATCCCAACCGCTTACCTGAGGCTCCG 60
DB 291 ATGTGGACATGAGGAGCCCTGACAACTGATCCCAACCGCTTACCTGAGGCTCCG 350
QY 61 AAGCCTCGGACTGCGACAGCAAAAGCTGACGCGCGCGGCTGAGCTGCGCTGCGCC 120
DB 351 AAGCCTCGGACTGCGACAGCAAAAGCTGACGCGCGCGGCTGAGCTGCGCTGCGCC 410
QY 121 GGGCTGCAAGGCTGCGGAGCTCCGCGCAAGAGCTGCTGAACTTCCACAGCTGTGT 180
DB 411 GGGCTGCAAGGCTGCGGAGCTCCGCGCAAGAGCTGCTGAACTTCCACAGCTGTGT 470
QY 181 GAGGACAGCCCATCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 471 GAGGACAGCCCATCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
QY 241 CGCAAGCGGCAACCTTCTAGAGAGCTGCAAACTGCGAGCTGCGAGAGAGAGCC 300
DB 531 CGCAAGCGGCAACCTTCTAGAGAGCTGCAAACTGCGAGCTGCGAGAGAGAGCC 590
QY 301 ACCAAAGACAGCGCGCTGCAAGGCGCTGCGAGCTGCGAGAGAGAGAGAGAGAG 360
DB 591 ACCAAAGACAGCGCGCTGCAAGGCGCTGCGAGCTGCGAGAGAGAGAGAGAGAG 650
QY 361 AACCCGCAACCTTCTGAGCAGCGCTGCGAGCTGCGAGAGAGAGAGAGAGAGAG 420
DB 651 AACCCGCAACCTTCTGAGCAGCGCTGCGAGCTGCGAGAGAGAGAGAGAGAGAG 710
QY 421 GAAAGAGAGAGCTGCGAGCTGCGAGAGCTGCGAGAGCTGCGAGAGAGAGAGAG 480
DB 711 GAAAGAGAGAGCTGCGAGCTGCGAGAGCTGCGAGAGCTGCGAGAGAGAGAGAG 770
QY 481 CAGCCCTTTAAGGATTTGCTGACCGAGCGCTTCTAGCAAAAGTTTCTGAGAGAGAG 540
DB 771 CAGCCCTTTAAGGATTTGCTGACCGAGCGCTTCTAGCAAAAGTTTCTGAGAGAGAG 830
QY 541 TTGAGATGACACAGTGTGACAAAGTACTTCACTAGATTGCTGAGAGAGAGAGAG 600
DB 831 TTGAGATGACACAGTGTGACAAAGTACTTCACTAGATTGCTGAGAGAGAGAGAG 890
QY 601 GGTGTTGGAGAGTATGCTGCTGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 891 GGTGTTGGAGAGTATGCTGCTGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 950
QY 661 AAATGAGCAAG 720

DB 951 AAATGAGCAAG 1010
QY 721 GAAATCTTGGAG 780
DB 1011 GAAATCTTGGAG 1070
QY 781 AAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 1071 AAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1130
QY 841 TACAACTGAG 900
DB 1131 TACAACTGAG 1190
QY 901 GCTGTTGGAG 960
DB 1191 GCTGTTGGAG 1250
QY 961 AATGCTGCTGAG 1020
DB 1251 AATGCTGCTGAG 1310
QY 1021 ATGAG 1080
DB 1311 ATGAG 1370
QY 1081 ATCTTAATGAG 1140
DB 1371 ATCTTAATGAG 1430
QY 1141 ATTATGAAATGAG 1200
DB 1431 ATTATGAAATGAG 1490
QY 1201 GAGAGATCTGAG 1260
DB 1491 GAGAGATCTGAG 1550
QY 1261 GAG 1320
DB 1551 GAG 1610
QY 1321 AGCAG 1380
DB 1611 AGCAG 1670
QY 1381 CGCTGAG 1440
DB 1671 CGCTGAG 1730
QY 1441 AAGAGATCTGAG 1500
DB 1731 AAGAGATCTGAG 1790
QY 1501 GATTAAG 1560
DB 1791 GATTAAG 1850
QY 1561 ATTATGAG 1620
DB 1851 ATTATGAG 1910
QY 1621 GAGGATTAATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1911 GAGGATTAATTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940

RESULT 2
AB086178
ID AB086178 standard; DNA; 1662 BP.
XX
AC AB086178;

	Query Match	99.8%;	Score 1655.8;	DB 6;	Length 1662;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 1657;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0
CC	trachea, thymus, lymph node and muscular system, obesity, anorexia,				
CC	growth abnormalities, and alleviation of precocious puberty. The				
CC	sequences given in records AB06130-AB06184 represent novel human cDNA's				
CC	of the invention				
XX					
Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;					
QY	1 ATGTGGAGACATGGGGGCGCCCTGGACACACCTGATGTGGCCACACCGCTTACTCTGGACGGCCGG 60				
DB	1 ATGTGGACATGGGGGCGCCCTGGACACACCTGATGTGGCCACACCGCTTACTCTGGACGGCCGG 60				
QY	61 AAGCCTTGAGACTGCGACACACAAAGAGCTGACCGGGCGGCGCTGAGCCTTGGCCCTTGGCC 120				
DB	61 AAGCCTTGAGACTGCGACACACAAAGAGCTGACCGGGCGGCGCTGAGCCTTGGCCCTTGGCC 120				
QY	121 GGGGTGACAGGGGTGCGGGGAGCTCCGCGACAGACTGTCTCCCTGAACTTCCACAGCTGTGT 180				
DB	121 GGGGTGACAGGGGTGCGGGGAGCTCCGCGACAGACTGTCTCCCTGAACTTCCACAGCTGTGT 180				
QY	181 GAGGACAGCCCATCGGTGCGCCTCTTCCTCGGACCTTCTACGACCAAGTGGCCACGTTTC 240				
DB	181 GAGGACAGCCCATCGGTGCGCCTCTTCCTCGGACCTTCTACGACCAAGTGGCCACGTTTC 240				
QY	241 CGCAGAGCGGCAACTTTCCTAGAGGACGTGACAGACTGGAGCTGGCCGAGAGGGACCC 300				
DB	241 CGCAGAGCGGCAACTTTCCTAGAGGACGTGACAGACTGGAGCTGGCCGAGAGGGACCC 300				
QY	301 ACCAAGACACGCGCGTCGAGGGGGTGGTGGCCACTGTGTGGAGTGGCTTGGCCCGGG 360				
DB	301 ACCAAGACACGCGCGTCGAGGGGGTGGTGGCCACTGTGTGGAGTGGCTTGGCCCGGG 360				
QY	361 AACCCTGACACCTTCTCTACGCTCAGGCGGTGGGCGACCAAGTGGCCACAGCCACCACTGAG 420				
DB	361 AACCCTGACACCTTCTCTACGCTCAGGCGGTGGGCGACCAAGTGGCCACAGCCACCACTGAG 420				
QY	421 GAAGAGCGAGTGGCTGACGTACCTGTCCGACAGGCTGAGGCCATGGCTTCTTGGCAAGAG 480				
DB	421 GAAGAGCGAGTGGCTGACGTACCTGTCCGACAGGCTGAGGCCATGGCTTCTTGGCAAGAG 480				
QY	481 CAGCCTTTAAGATTTTCTGTGACAGGGCCTTCTACACAAAGTTTCTGATGGAAATC 540				
DB	481 CAGCCTTTAAGATTTTCTGTGACAGGGCCTTCTACACAAAGTTTCTGATGGAAATC 540				
QY	541 TTGAGATGACACCAAGTGTGACACAAATCTTCACTAGTTGAGTTCAGAGTCTGGGAAAGGT 600				
DB	541 TTGAGATGACACCAAGTGTGACACAAATCTTCACTAGTTGAGTTCAGAGTCTGGGAAAGGT 600				
QY	601 GGTTTTGGGGAGGTATGTGCGGTCCAGGTGAGAAACCTGGGAAGTATGCTCTGTAG 660				
DB	601 GGTTTTGGGGAGGTATGTGCGGTCCAGGTGAGAAACCTGGGAAGTATGCTCTGTAG 660				
QY	661 AAATGTGACAGAAAGCGGCTGAGAAAGAAAGGTGGCAGAAAGTGGCTTCTTGGAAAG 720				
DB	661 AAATGTGACAGAAAGCGGCTGAGAAAGAAAGGTGGCAGAAAGTGGCTTCTTGGAAAG 720				
QY	721 GAAATCTTGGAGAAAGTCAAGAGCCTCTTCAATGTCTCTCTGGCCTATGCTTGGAGAC 780				
DB	721 GAAATCTTGGAGAAAGTCAAGAGCCTCTTCAATGTCTCTCTGGCCTATGCTTGGAGAC 780				
QY	781 AAGACCCATCTGTCGCTTGTATAGCTGAGAAATGGGGAGAACCTCAAGTTCCACATC 840				
DB	781 AAGACCCATCTGTCGCTTGTATAGCTGAGAAATGGGGAGAACCTCAAGTTCCACATC 840				
QY	841 TACAACTGTGGGCACTGCTGTGGCTTGAACATGAGCGGGTGAATCTTTTACTGGGCCACAGTA 900				
DB	841 TACAACTGTGGGCACTGCTGTGGCTTGAACATGAGCGGGTGAATCTTTTACTGGGCCACAGTA 900				
QY	901 GCGTGTGGAGTGTGCACTTCATGAACTGGGCACTGCTTACCGGACATGAAAGCTGAG 960				

XX Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual
 PT signaling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.

PS Example 4; Page 45-46; 61pp; English.

XX The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signaling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC blindness), pineal gland activity (e.g., chronobiological desynchrony,
 CC depression, anxiety, mental foginess, memory loss, headaches, fatigue,
 CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
 CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
 CC preparation of a medicament for treating a condition or disease related
 CC to cone photoreceptor visual signaling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for
 CC individuals with such disorders. The present sequence is human GRK7 cDNA

SQ Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Query Match 99.8%; Score 1655.8; DB 6; Length 1662;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGTGACATGCGGGCCCTTGACACACCTGATCCGCAACCGGCTTACGTGACGGCCGGG 60
 DB 1 ATGTGTGACATGCGGGCCCTTGACACACCTGATCCGCAACCGGCTTACGTGACGGCCGGG 60
 QY 61 AAGCCTTGAGAGCTGCGACAGCAAAAGAGCTGACGCGCGGCGTACGCTTGGCCCTGCGCC 120
 DB 61 AAGCCTTGAGAGCTGCGACAGCAAAAGAGCTGACGCGCGGCGTACGCTTGGCCCTGCGCC 120
 QY 121 GGGCTGACGAGCTGCGGAGCTCCGCCAAGAGCTGTCCCTGAACTTCCACAGCTGTGT 180
 DB 121 GGGCTGACGAGCTGCGGAGCTCCGCCAAGAGCTGTCCCTGAACTTCCACAGCTGTGT 180
 QY 181 GAGCAGACACCCATGATGTCGCCCTCTTCCGTGATCTTCTGACGAGTCCCAAGTTC 240
 DB 181 GAGCAGACACCCATGATGTCGCCCTCTTCCGTGATCTTCTGACGAGTCCCAAGTTC 240
 QY 241 CGCAAGCGCGCAACCTTCTTACGAGAGCTGCAAGAGCTGAGAGCTGAGAGAGAGAGAG 300
 DB 241 CGCAAGCGCGCAACCTTCTTACGAGAGCTGCAAGAGCTGAGAGCTGAGAGAGAGAGAG 300
 QY 301 ACCAAGAGAGCGGCTGACGAGGCTGTGTGCACTTGTGCGATGTCCTGAGTCCCTGCGGG 360
 DB 301 ACCAAGAGAGCGGCTGACGAGGCTGTGTGCACTTGTGCGATGTCCTGAGTCCCTGCGGG 360
 QY 361 AACCAGCAACCTTCTTCTTACGAGAGCTGCGCAACAGAGCCCAAGAGCCCAAGTGA 420
 DB 361 AACCAGCAACCTTCTTCTTACGAGAGCTGCGCAACAGAGCCCAAGAGCCCAAGTGA 420
 QY 421 GAAGAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
 DB 421 GAAGAGAGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
 QY 481 CAGCCCTTTAAGATTTGTGACCAAGCTGCTTCAACAGCAAGTTTCTGAGTGAAGATCTC 540
 DB 481 CAGCCCTTTAAGATTTGTGACCAAGCTGCTTCAACAGCAAGTTTCTGAGTGAAGATCTC 540

QY 541 TTGAGAGCAACCAAGTGTGACAGAGTACTTCACTGATGTTGAGAGTCTGGGAAAGT 600
 DB 541 TTGAGATGCAACCAAGTGTGACAGAGTACTTCACTGATGTTGAGAGTCTGGGAAAGT 600
 QY 601 GGTTTGGGAGAGTATGTGTCGTCAGGTGAAAGCACTGGGAGATGTATGCTTGAAG 660
 DB 601 GGTTTGGGAGAGTATGTGTCGTCAGGTGAAAGCACTGGGAGATGTATGCTTGAAG 660
 QY 661 AAACCTGACAAAGCGGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 661 AAACCTGACAAAGCGGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 721 GAATCTTGAAGAGTACAGCAGCCCTTCAATGTCTCTGAGCTTGAAGC 780
 DB 721 GAATCTTGAAGAGTACAGCAGCCCTTCAATGTCTCTGAGCTTGAAGC 780
 QY 781 AAGACCATCTGCTGCTTGTGATGAGCCTGATGATGAGGAGAGAGAGAGAGAGAGAG 840
 DB 781 AAGACCATCTGCTGCTTGTGATGAGCCTGATGATGAGGAGAGAGAGAGAGAGAGAG 840
 QY 841 TACAGCGTGGGAGCGGCTGAGACATGAGCGGAGTATCTTTTACTCGGCGAGATA 900
 DB 841 TACAGCGTGGGAGCGGCTGAGACATGAGCGGAGTATCTTTTACTCGGCGAGATA 900
 QY 901 GCTGTGAGATGCTGACCTTCAATGAACTGCGCATGCTATGCGGACATGAAGCTGAG 960
 DB 901 GCTGTGAGATGCTGACCTTCAATGAACTGCGCATGCTATGCGGACATGAAGCTGAG 960
 QY 961 AATGTCTTGTGATGACCTTGGGAACTGCAAGTATATGATCTTGGGAGCTGGGCTGAG 1020
 DB 961 AATGTCTTGTGATGACCTTGGGAACTGCAAGTATATGATCTTGGGAGCTGGGCTGAG 1020
 QY 1021 ATGAAGGAGTGGCAAGCCCATACCCAGAGGCTGGAACCAATGATGATGATGATGATG 1080
 DB 1021 ATGAAGGAGTGGCAAGCCCATACCCAGAGGCTGGAACCAATGATGATGATGATGATG 1080
 QY 1081 ATCTTAATGAGAAAGTAAAGTATTCATCTGTGAGCTGTTGCTCAGTGGAGTGCAGC 1140
 DB 1081 ATCTTAATGAGAAAGTAAAGTATTCATCTGTGAGCTGTTGCTCAGTGGAGTGCAGC 1140
 QY 1141 ATTTATGAATGTTGCTGAGCAAGCAACATTCGAAGTTTCAAGGAAAGAGTCAAGTAA 1200
 DB 1141 ATTTATGAATGTTGCTGAGCAAGCAACATTCGAAGTTTCAAGGAAAGAGTCAAGTAA 1200
 QY 1201 GAGGATCTGAGCAAGAACTCTGCAAGAGAGTCAATTCAGATGATTAATCTTACA 1260
 DB 1201 GAGGATCTGAGCAAGAACTCTGCAAGAGAGTCAATTCAGATGATTAATCTTACA 1260
 QY 1261 GAGGAGCAAAAGATATTTGAGAGCTTCTTGGCTAAGAAACAGAGCAAGCTTGA 1320
 DB 1261 GAGGAGCAAAAGATATTTGAGAGCTTCTTGGCTAAGAAACAGAGCAAGCTTGA 1320
 QY 1321 AGCAGAGAAAGTGTGATGATCCAGAGAAACATCAATCTTTAAAGATCAACTTCT 1380
 DB 1321 AGCAGAGAAAGTGTGATGATCCAGAGAAACATCAATCTTTAAAGATCAACTTCT 1380
 QY 1381 GGCCTGAGAGCTGCAATTAAGACCCCATTTGTGCAAGACCTTCAAGTGTATATCC 1440
 DB 1381 GGCCTGAGAGCTGCAATTAAGACCCCATTTGTGCAAGACCTTCAAGTGTATATCC 1440
 QY 1441 AAGACATGCTGAAATGATGATTTCTGAGGTGCGGAGGAGTGAATTTATGACAAA 1500
 DB 1441 AAGACATGCTGAAATGATGATTTCTGAGGTGCGGAGGAGTGAATTTATGACAAA 1500
 QY 1501 GATTAAGAGTCTTCAAAAACCTTTGCAAGAGTGTGCTTATAGCATGAGAGAGAA 1560
 DB 1501 GATTAAGAGTCTTCAAAAACCTTTGCAAGAGTGTGCTTATAGCATGAGAGAGAA 1560
 QY 1561 ATTATAGAAACGGGAGCTGTTTGAAGAACTGATGATGATGATGATGATGATGATG 1620
 DB 1561 ATTATAGAAACGGGAGCTGTTTGAAGAACTGATGATGATGATGATGATGATGATG 1620
 QY 1621 GAGGATTAATTCATCAAGTCTGCGGTGTGTTTATTTG 1655

DB 1621 GAGGGTATTGATCCAGATCGGCGTGTGTTATTG 1659
|||||
RESULT 5
AB256943
ID AB256943 standard; DNA; 1761 BP.
XX
AC AB256943;
XX
XX 04-APR-2003 (first entry)
XX
DE Human gene sequence relative to the invention # SEQ ID 11.
XX
XX Human; heart disease; cancer; omentopathy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..1687
FT /tag= a
XX
XX WO2002103020-A1.
XX
XX 27-DEC-2002.
XX
XX 14-JUN-2002; 2002MO-JP005942.
XX
XX 15-JUN-2001; 2001JP-00182654.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Koyama N, Tanida S, Yamamoto K;
XX
XX WPI; 2003-157045/15.
XX
XX P-PSDB; ABP60079.
XX
XX Novel disease-associated gene of the RGS gene family and its product,
PT applicable in diagnosis of and screening for drugs for heart diseases,
PT cancers and omentopathy.
XX
XX Example 3; Page 85-86; 96pp; Japanese.
XX
XX The invention relates to a novel disease associated gene and its uses.
CC The gene and its encoded protein are useful for diagnosis of and
CC screening for drugs for heart diseases, cancers and omentopathy. The
CC current sequence represents a human gene sequence relative to the
CC invention
XX
XX Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
SQ
Query Match 99.8%; Score 1655.8; DB 7; Length 1761;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGTGTGACATGGGGGCTCTGAGAACCTGATGCGCAACCGCTTACTGAGGCCCGG 60
DB 26 ATGGGAGCATGGGGGCTCTGAGAACCTGATGCGCAACCGCTTACTGAGGCCCGG 85
QY 61 AAGCCCTGAGCTGCGACGACAAAGAGCTGCGAGCGGGGGGTAGCTGGCCCTGCGC 120
DB 86 AAGCCCTGAGCTGCGACGACAAAGAGCTGCGAGCGGGGGGTAGCTGGCCCTGCGC 145
QY 121 GGGCTGCGAGGCTGCGAGCTGCGAGAACCTGCTGATGACTTCCACAGCTGTGT 180
DB 146 GGGCTGCGAGGCTGCGAGCTGCGAGAACCTGCTGATGACTTCCACAGCTGTGT 205
QY 181 GAGGAGGAGCCATGCTGCTGCGAGCTGCTGATGACTTCCACAGCTGTGT 240
DB 206 GAGGAGGAGCCATGCTGCTGCGAGCTGCTGATGACTTCCACAGCTGTGT 265
QY 241 CGAAGGCGGCACTTCTAGAGAGCTGCGAGCTGCGAGCTGCGAGGAGGAGGCC 300
|||||

DB 266 CGCAGGCGGCACTTCTAGAGAGCTGCAAACTGGAGCTGGCCGAGGAGGCC 325
QY 301 ACCAAGACAGCGCGTGTGAGGGCTGTGTGCACTTGTGTGAGTGCCTCTGCCGCGG 360
DB 326 ACCAAGACAGCGCGTGTGAGGGCTGTGTGCACTTGTGTGAGTGCCTCTGCCGCGG 385
QY 361 AACCCGCAACCTTCTGAGCGCGTGTGCACTTGTGTGAGTGCCTCTGCCGCGG 420
DB 386 AACCCGCAACCTTCTGAGCGCGTGTGCACTTGTGTGAGTGCCTCTGCCGCGG 445
QY 421 GAAAGCGAGTGTGTGAGCGCTGCGAAGGCTGAGGCGCTTCTTGTGAGAG 480
DB 446 GAAAGCGAGTGTGTGAGCGCTGCGAAGGCTGAGGCGCTTCTTGTGAGAG 505
QY 481 GAGCCCTTTAAGATTTGTGTGAGCGCTTCTTGTGAGAG 540
DB 506 GAGCCCTTTAAGATTTGTGTGAGCGCTTCTTGTGAGAG 565
QY 541 TTGAGATGCAACAGTGTGCAAGTACTTCACTGAGTTGAGAGTGTGAGAG 600
DB 566 TTGAGATGCAACAGTGTGCAAGTACTTCACTGAGTTGAGAGTGTGAGAG 625
QY 601 GGTTTGGGAGATATGTGCGTCCAGTGAAGAACTGGAGAGATGTATGCTGTAG 660
DB 626 GGTTTGGGAGATATGTGCGTCCAGTGAAGAACTGGAGAGATGTATGCTGTAG 685
QY 661 AAATGTGACAAAGACCGGTGAGAGAGAGTGTGAGAGAGTGTGTGAGAG 720
DB 686 AAATGTGACAAAGACCGGTGAGAGAGAGTGTGAGAGAGTGTGTGAGAG 745
QY 721 GAAATCTTGGAGAGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 780
DB 746 GAAATCTTGGAGAGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 805
QY 781 AAGACCATCTCTGCTTGTGATGAGCTGTGATGAGTGTGAGAGAGTGTGTGAGAG 840
DB 806 AAGACCATCTCTGCTTGTGATGAGCTGTGATGAGTGTGAGAGAGTGTGTGAGAG 865
QY 841 TACAGCTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 900
DB 866 TACAGCTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 925
QY 901 GCTGTGAGAGTGTGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 960
DB 926 GCTGTGAGAGTGTGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 985
QY 961 AATGTCTTGTGATGAGCTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1020
DB 986 AATGTCTTGTGATGAGCTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1045
QY 1021 ATGAAGGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1080
DB 1046 ATGAAGGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1105
QY 1081 ATCTTAATGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1140
DB 1106 ATCTTAATGAGAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1165
QY 1141 ATTTATGAAATGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1200
DB 1166 ATTTATGAAATGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1225
QY 1201 GAGGATCTGAAGCAAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1260
DB 1226 GAGGATCTGAAGCAAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1285
QY 1261 GAGGATCTGAAGCAAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1320
DB 1286 GAGGATCTGAAGCAAGAGTGTGTGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1345
QY 1321 AGGAGAGAGAGTGTGTGATGATGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1380
DB 1346 AGGAGAGAGAGTGTGTGATGATGAGAGAGTGTGTGAGAGAGTGTGTGAGAG 1405

QY 1381 CGCCGAGACCTGGCTTAATGAAACCCCACTTTGGCCAGCCCTTGAAGTTATGCC 1440
 DB 1406 CGCCGAGACCTGGCTTAATGAAACCCCACTTTGGCCAGCCCTTGAAGTTATGCC 1465
 QY 1441 AAGGACATCGCTGAATTTGATGATTTCTCGAGAGTTGGGGGGGGAATTTATGACAAA 1500
 DB 1466 AAGGACATCGCTGAATTTGATGATTTCTCGAGAGTTGGGGGGGGAATTTATGACAAA 1525
 QY 1501 GATAGACAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTTATAGATGCGAGAGAAA 1560
 DB 1526 GATAGACAGTTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTTATAGATGCGAGAGAAA 1585
 QY 1561 ATTATAGAAAACGAGCTGTTTGAAGAACTGATGACCCCAACAACTACGAGTTGTAG 1620
 DB 1586 ATTATAGAAAACGAGCTGTTTGAAGAACTGATGACCCCAACAACTACGAGTTGTAG 1645
 QY 1621 GAGGTAATTCATGCAAGTCTGGCGGTGTTGTATG 1659
 DB 1646 GAGGTAATTCATGCAAGTCTGGCGGTGTTGTATG 1684

RESULT 6
 ADC39221
 ID ADC39221 standard; cDNA; 1821 BP.
 AC ADC39221;
 XX
 DT 18-DEC-2003 (first entry)
 DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
 KW ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
 KW antilipemic; neurotrophic; neuroprotective; immunostimulant;
 KW antiparkinsonian; anti-HIV; antiaesthetic; antiinflammatory; hypotensive;
 KW antidiabetic; cancer; lymphoma; uterine cancer; prostate cancer;
 KW diabetes; obesity; anorexia; wasting disorder; Alzheimer's disease;
 KW dyslipidemia; anorexia; wasting disorder; Alzheimer's disease;
 KW Parkinson's disease; cachexia; cardiomyopathy; AIDS; asthma;
 KW Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;
 KW hemophilia; graft-versus-host disease;
 KW Albright hereditary osteodystrophy.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..1732
 FT /tag= a
 XX
 PN WO2003010327-A2.
 PD
 XX
 PD 06-FEB-2003.
 PF 02-MAY-2002; 2002WO-US014199.
 XX
 XX 02-MAY-2001; 2001US-0288063P.
 PR 03-MAY-2001; 2001US-0288395P.
 PR 07-MAY-2001; 2001US-0289087P.
 PR 09-MAY-2001; 2001US-0289817P.
 PR 09-MAY-2001; 2001US-0289818P.
 PR 11-MAY-2001; 2001US-0290194P.
 PR 14-MAY-2001; 2001US-0290753P.
 PR 15-MAY-2001; 2001US-0291181P.
 PR 16-MAY-2001; 2001US-0291243P.
 PR 18-MAY-2001; 2001US-0292001P.
 PR 21-MAY-2001; 2001US-0292374P.
 PR 22-MAY-2001; 2001US-0292587P.
 PR 23-MAY-2001; 2001US-0293107P.
 PR 25-MAY-2001; 2001US-0293747P.
 PR 29-MAY-2001; 2001US-0294109P.
 PR 29-MAY-2001; 2001US-0294110P.
 PR 30-MAY-2001; 2001US-0294434P.
 PR 31-MAY-2001; 2001US-0294827P.

PR 12-JUL-2001; 2001US-0304879P.
 PR 31-JUL-2001; 2001US-0308901P.
 PR 14-AUG-2001; 2001US-0312270P.
 PR 17-AUG-2001; 2001US-0313416P.
 PR 10-SEP-2001; 2001US-0318463P.
 PR 27-SEP-2001; 2001US-0325683P.
 PR 18-OCT-2001; 2001US-0330292P.
 PR 28-NOV-2001; 2001US-0338737P.
 PR 03-DEC-2001; 2001US-0336909P.
 PR 03-DEC-2001; 2001US-0337552P.
 PR 21-FEB-2002; 2002US-0359245P.
 PR 01-MAY-2002; 2002US-00136826.
 XX
 PA (CUBA-) CURAGEN CORP.
 XX
 PI Miller CE, Kekuda R, Malysankar UM, Li L, Pena CE, Splek KA;
 PI Gorman L, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerkow BD;
 PI Paturajan M, Anderson JW, Mezes PS, Peyman JA, Macdougall JR;
 PI Padigaru M, Rastelli L, Shenoy SG, Gerlach VL, Shinkens RA, Zhong M;
 PI Edinger SR, Ellerman K;
 XX
 DR MPI. 2003-239445/23.
 DR P-PSDB; ADC39222.
 XX
 PT New NOVX polypeptides and polynucleotides, useful in gene therapy,
 PT particularly for treating or preventing a syndrome associated with a
 PT human disease e.g., diabetes, obesity, cancer, Alzheimer's disease,
 PT hypertension or hemophilia.
 XX
 PS Claim 20; SEQ ID NO 165; 748bp; English.
 XX
 CC The invention relates to new isolated NOVX polypeptides, the genes
 CC encoding them or sequences having at least 95% identity to the amino acid
 CC or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
 CC particularly in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, which includes a pathology associated
 CC with NOVX polypeptide. The NOVX polypeptide is particularly useful for
 CC treating, preventing or alleviating pathology associated with NOVX
 CC polypeptide in a mammal, e.g., a human. The NOVX nucleic acid and
 CC polypeptide are especially useful for treating or preventing e.g.,
 CC diabetes, obesity, cancers (e.g., lymphoma, uterine cancer or prostate
 CC cancer), dyslipidemia, anorexia, wasting disorders, Alzheimer's disease,
 CC Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
 CC disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
 CC graft-versus-host disease or Albright hereditary osteodystrophy. The DNA
 CC encoding the protein is useful in gene therapy for treating the above
 CC conditions. These are also useful in developing powerful assay system for
 CC functional analysis of various human disorders, as well as in diagnostic
 CC applications. This sequence represents one of the NOVX genes of the
 CC invention.
 CC
 SQ Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;
 Query Match 99.8%; Score 1655.8; DB 9; Length 1821;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAGGTGACATGAGGGGCGCTGAGCAACCTGATGCGCAACCGCTTACCTGAGCGCGG 60
 DB 73 AAGGTGACATGAGGGGCGCTGAGCAACCTGATGCGCAACCGCTTACCTGAGCGCGG 112
 QY 61 AAGCTCTGAGCTGCGACAGCAAGAGCTGCGAGCGCGCGGTAGCTGGCCCTGCCC 120
 DB 133 AAGCTCTGAGCTGCGACAGCAAGAGCTGCGAGCGCGCGGTAGCTGGCCCTGCCC 192
 QY 121 GGGCTGCAAGGCTGCGCGAGAGTCTCCGCAAGCTGCTCCGAACTTCCACAGCCTGTGT 180
 DB 193 GGGCTGCAAGGCTGCGCGAGAGTCTCCGCAAGCTGCTCCGAACTTCCACAGCCTGTGT 252
 QY 181 GAGGACAGAGCCCATGCGGTGCGCGCTCTTCCGTAATTCTAGCCAGAGTCCAGGTTTC 240
 DB 253 GAGGACAGAGCCCATGCGGTGCGCGCTCTTCCGTAATTCTAGCCAGAGTCCAGGTTTC 312

QY	901	GCCTTGGAATGCTGACCTTCATGAACTCGGCATGCTCTATGCGGAGCATGAAAGCCTGAG	960
Db	1254	GCCTGTGGGATGCTGACCTTCATGAACTCGGCATGCTCTATGCGGAGCATGAAAGCCTGAG	1313
QY	961	AATGTGCTTCGGATGAACCTCGGCACTGCAAGTATATGACCTTGCGGCTGAGCGTGGAG	1020
Db	1314	AATGTGCTTCGGATGAACCTCGGCACTGCAAGTATATGACCTTGCGGCTGAGCGTGGAG	1373
QY	1021	ATGAAAGGTGGCAAGCCATCACCCAGAGGCTGAAACCAATGTTTCATGCTCTCTAG	1080
Db	1374	ATGAAAGGTGGCAAGCCATCACCCAGAGGCTGAAACCAATGTTTCATGCTCTCTAG	1433
QY	1081	ATCTCTAATGCAAAAGGTAAAGTTATTCCTTCTGCTGGACCTGGTTGCGCATGAGTACAGC	1140
Db	1434	ATCTCTAATGCAAAAGGTAAAGTTATTCCTTCTGCTGGACCTGGTTGCGCATGAGTACAGC	1493
QY	1141	ATTATGTAATATGCTGTGCGACGACACCATTCACAAATTAACAGAAAAAGTCAGTAAA	1200
Db	1494	ATTATGTAATATGCTGTGCGACGACACCATTCACAAATTAACAGAAAAAGTCAGTAAA	1553
QY	1201	GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAATTCACAGATGATCTTGCA	1260
Db	1554	GAGGATCTGAAGCAAGAACTCTGCAAGACGAGTCAATTCACAGATGATCTTGCA	1613
QY	1261	GAGGAAGCAAAAGATTTTGGCAGGCTCTTCCTGGCTAAGAAACAGAGCAACCTTAGGA	1320
Db	1614	GAGGAAGCAAAAGATTTTGGCAGGCTCTTCCTGGCTAAGAAACAGAGCAACCTTAGGA	1673
QY	1321	AGCAGAGAAAAGTCTGATATCCAGAAAACATCATTTCTTTAAACGATCACTTCT	1380
Db	1674	AGCAGAGAAAAGTCTGATATCCAGAAAACATCATTTCTTTAAACGATCACTTCT	1733
QY	1381	CGCTGGAAGCTGGCTTAATGAAACCCCATTTGGCGACACCCCTCAGTGGTTATGCG	1440
Db	1734	CGCTGGAAGCTGGCTTAATGAAACCCCATTTGGCGACACCCCTCAGTGGTTATGCG	1793
QY	1441	AAAGACATGCTGAATATGATATTTCTCTGAGGTTGCGGCGGTGGAAATTGATGACAA	1500
Db	1794	AAAGACATGCTGAATATGATATTTCTCTGAGGTTGCGGCGGTGGAAATTGATGACAA	1853
QY	1501	GATAGCAGTCTTTCAAAACTTTGCGACAGTGCTGTCTCTATGACATGGCAGAGAA	1560
Db	1854	GATAGCAGTCTTTCAAAACTTTGCGACAGTGCTGTCTCTATGACATGGCAGAGAA	1913
QY	1561	ATTATAGAAACGGGACCTGTTGAGGAATGGAATGACCCCAACAGACTTACGGGTGGAG	1620
Db	1914	ATTATAGAAACGGGACCTGTTGAGGAATGGAATGACCCCAACAGACTTACGGGTGGAG	1973
QY	1621	GAGGTAATTCATCCAGAGTCTGGCTGTGTTGTTGTTATTTG	1659
Db	1974	GAGGTAATTCATCCAGAGTCTGGCTGTGTTGTTGTTATTTG	2012
RESULT 8			
ACCC4827			
ID	ACCC4827	standard; cDNA; 3186 BP.	
XX	ACCC4827;		
DT	04-JUN-2003	(first entry)	
DE	Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.		
XX			
KM	Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;		
KM	neuroprotective; mototropic; cardiovascular; anti-parkinsonian; cardiac;		
KM	vasotrophic; antiaesthetic; gene therapy; cancer; diabetes; CNS disorder;		
KM	central nervous system disorder; cardiovascular disorder; asthma; COPD;		
KM	chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;		
KM	Alzheimer's disease; Parkinson's disease; congenital heart failure;		
KM	myocardial infarction; ischaemic disease; hypertensive vascular disease;		
KM	gene; ss.		

QY	361	AAACCCGAAACCCCTTCTCAGCAGAGCGCTGGCCACAATGTCGAAAGCAACCACTGAG	420
DB	445	AAACCCGAAACCCCTTCTCAGCAGAGCGCTGGCCACAATGTCGAAAGCAACCACTGAG	504
QY	421	GAAGAGGAGATGGCTGCGAGTGAACGCTGGCGAAAGCTGAGAGCCATGAGCTTTCTTGGTAAG	480
DB	505	GAAGAGGAGATGGCTGCGAGTGAACGCTGGCGAAAGCTGAGAGCCATGAGCTTTCTTGGTAAG	564
QY	481	CAGCCCTTTAAGGATTTTGTGACCAAGCCCTTCTCAAGCAAGTTTCTGAGTGGAAAATC	540
DB	565	CAGCCCTTTAAGGATTTTGTGACCAAGCCCTTCTCAAGCAAGTTTCTGAGTGGAAAATC	624
QY	541	TTCCAGATGGAACCAAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAAGT	600
DB	625	TTCCAGATGGAACCAAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAAAAGT	684
QY	601	GGTTTTGGGAGAGTATGNGCCGTCCAGGTCGAAAAACATCGGGAGATGATATCCCTGTAAG	660
DB	685	GGTTTTGGGAGAGTATGNGCCGTCCAGGTCGAAAAACATCGGGAGATGATATCCCTGTAAG	744
QY	661	AAACTGCAACAGAACCGCTGAAAGAAAGATGTGCGAAGATAGCTCTCTTGGAAGAG	720
DB	745	AAACTGCAACAGAACCGCTGAAAGAAAGATGTGCGAAGATAGCTCTCTTGGAAGAG	804
QY	721	GAATCTTGGAAAAGTCAAGCAAGCCCTTCAATGTCTCTCTGCGCTATGACCTTTGAGAGC	780
DB	805	GAATCTTGGAAAAGTCAAGCAAGCCCTTCAATGTCTCTCTGCGCTATGACCTTTGAGAGC	864
QY	781	AAGACCCATCTGTGCTCTGTCATGAGCCCTGATGTAATAGGGGAGACCTCAAGTTCACATC	840
DB	865	AAGACCCATCTGTGCTCTGTCATGAGCCCTGATGTAATAGGGGAGACCTCAAGTTCACATC	924
QY	841	TACACGTGCGACGCGCTGGCCCTGGACATGAGCCGCGTATCTTTACTCGGCCACATA	900
DB	925	TACACGTGCGACGCGCTGGCCCTGGACATGAGCCGCGTATCTTTACTCGGCCACATA	984
QY	901	GCCCTGGGAGATGTCGCACTCTCAATGAACTGGCATCTCTATGCGGACATGAAAGCTTGAG	960
DB	985	GCCCTGGGAGATGTCGCACTCTCAATGAACTGGCATCTCTATGCGGACATGAAAGCTTGAG	1044
QY	961	AATGTCTTCTGAGATGACCTCGGCAACATCGAGGTTATCTGAACCTGGGGGTGGCCCTGGAG	1020
DB	1045	AATGTCTTCTGAGATGACCTCGGCAACATCGAGGTTATCTGAACCTGGGGGTGGCCCTGGAG	1104
QY	1021	ATGAAGGCTGGCAAGCCCATACCCGAGAGGCTGGACCAATGTTAATAGGCTCTCGAG	1080
DB	1105	ATGAAGGCTGGCAAGCCCATACCCGAGAGGCTGGACCAATGTTAATAGGCTCTCGAG	1164
QY	1081	ATCCCTAATGGAAGAAAGGTAAGTTATCTCTATCTCTGTGACATGTGTTGCCATGGAGTCAGC	1140
DB	1165	ATCCCTAATGGAAGAAAGGTAAGTTATCTCTATCTCTGTGACATGTGTTGCCATGGAGTCAGC	1224
QY	1141	ATTATGAAATGATGTCTGTGACGAACCATTCACAAAGTTACAAGGAAAAGTCCAGTAATA	1200
DB	1225	ATTATGAAATGATGTCTGTGACGAACCATTCACAAAGTTACAAGGAAAAGTCCAGTAATA	1284
QY	1201	GAGGATCTGAAGCAAAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATCTTACA	1260
DB	1285	GAGGATCTGAAGCAAAAGAACTCTGCAAGACGAGTCAAAATTCAGCATGATTAATCTTACA	1344
QY	1261	GAGGAAAGCAAAAGATTTTGGAGGCTCTCTTGCGTAAAGAACAGAGACAACGTTAGGA	1320
DB	1345	GAGGAAAGCAAAAGATTTTGGAGGCTCTCTTGCGTAAAGAACAGAGACAACGTTAGGA	1404
QY	1321	AGCAGAGAAAAGTCTGATGATCCAGGAAACATATTTCTTTAAAAGATCACTTTCCT	1380
DB	1405	AGCAGAGAAAAGTCTGATGATCCAGGAAACATATTTCTTTAAAAGATCACTTTCCT	1464
QY	1381	CGCTCGGAAGCTGGCTTAATTGAAACCCCAATTTGTGCGACAGCCCTTCAAGTGTATTATCC	1440
DB	1465	CGCTCGGAAGCTGGCTTAATTGAAACCCCAATTTGTGCGAGACCCCTTCAAGTGTATTATCC	1524

Query Match	99.8%	Score 1655.4	DB 4	Length 1662
Best Local Similarity	99.8%	Ped. No. 0		
Matches 1656	Conservative 1	Mismatches 2	Indels 0	Gaps 0
1 ATGTGGACATATGGGGGCGCTGGACACCTATCTGCGCAACCGCCCTACTCTGACGGCCGG 60				
1 ATGTGGACATATGGGGGCGCTGGACACCTATCTGCGCAACCGCCCTACTCTGACGGCCGG 60				
61 AAGCCTCTGGAAGCTGCGACGACGAAAGAGCTGACGCGCGCGCGGTAGCCTGGCCCTGCC 120				
61 AAGCCTCTGGAAGCTGCGACGACGAAAGAGCTGACGCGCGCGCGGTAGCCTGGCCCTGCC 120				
121 GGGCTGACAGGCGCTGCGGGAGCTCCGCAAGACGTGCTCCGAACTTCCACAGGCTGTG 180				
121 GGGCTGACAGGCGCTGCGGGAGCTCCGCAAGACGTGCTCCGAACTTCCACAGGCTGTG 180				
121 GGGCTGACAGGCGCTGCGGGAGCTCCGCAAGACGTGCTCCGAACTTCCACAGGCTGTG 180				
181 GAGACGACCCCATCGGTGCGCGCCTCTTCCGAGACTTCTGAGCCACAGTGGCCACGTTG 240				
181 GAGACGACCCCATCGGTGCGCGCCTCTTCCGAGACTTCTGAGCCACAGTGGCCACGTTG 240				
241 CGCAAGCGCGCAACCTTCTTAAGAGACGTGACAGACTGGAGCTGCGCGACGAGAGACC 300				
241 CGCAAGCGCGCAACCTTCTTAAGAGACGTGACAGACTGGAGCTGCGCGACGAGAGACC 300				
301 ACCAAGAGAGCGGCTGACGAGGCGGTGTGGCACTGTGGAGTGGCCCTGCCCGGCG 360				
301 ACCAAGAGAGCGGCTGACGAGGCGGTGTGGCACTGTGGAGTGGCCCTGCCCGGCG 360				
301 ACCAAGAGAGCGGCTGACGAGGCGGTGTGGCACTGTGGAGTGGCCCTGCCCGGCG 360				
361 AACCCGCAACCTTCTCTACACGACGCGCTGACACCAAGTGCACAGAGACACCACTGAG 420				
361 AACCCGCAACCTTCTCTACACGACGCGCTGACACCAAGTGCACAGAGACACCACTGAG 420				
361 AACCCGCAACCTTCTCTACACGACGCGCTGACACCAAGTGCACAGAGACACCACTGAG 420				
421 GAAAGAGAGTGGCTGACGTGACGCTGCGCAAGCTGAGGCAATGGCTTTCTTGAAGAAG 480				
421 GAAAGAGAGTGGCTGACGTGACGCTGCGCAAGCTGAGGCAATGGCTTTCTTGAAGAAG 480				
421 GAAAGAGAGTGGCTGACGTGACGCTGCGCAAGCTGAGGCAATGGCTTTCTTGAAGAAG 480				
481 CAGCCCTTTAAGGATTTGTGACAGCGCCCTTCTTAAGCAATGTTCTGCAAGTGGAAATC 540				
481 CAGCCCTTTAAGGATTTGTGACAGCGCCCTTCTTAAGCAATGTTCTGCAAGTGGAAATC 540				
541 TTTCAGATGCAACAGATGTGACGAAAGTACTTCACTGAGTTCAAGATGTGCGGAAAGT 600				
541 TTTCAGATGCAACAGATGTGACGAAAGTACTTCACTGAGTTCAAGATGTGCGGAAAGT 600				
601 GGTTTTGGGAGGTATGTGCCCTTCAAGTGAAGAAACATCTGGGAGAGATGTGCTGTAG 660				
601 GGTTTTGGGAGGTATGTGCCCTTCAAGTGAAGAAACATCTGGGAGAGATGTGCTGTAG 660				
661 AATCTGACAAAGAGCGCTGAAAGAAAGTGGCGAAGATGCTCTCTTGAAGAAAG 720				
661 AATCTGACAAAGAGCGCTGAAAGAAAGTGGCGAAGATGCTCTCTTGAAGAAAG 720				
721 GAATCTTGGAGAGGTGACAGACCCCTTCAATGTCTCTCTGCGCTTATGCTTGAAGC 780				
721 GAATCTTGGAGAGGTGACAGACCCCTTCAATGTCTCTCTGCGCTTATGCTTGAAGC 780				
781 AAGACCATCTCTGCTTGTATGACCTGATGAATGAGGAGAGACCTTCAAGTCCACATC 840				
781 AAGACCATCTCTGCTTGTATGACCTGATGAATGAGGAGAGACCTTCAAGTCCACATC 840				
841 TACAACGTGGACAGCGGTGCTGACATGACCGGGTATCTTTACTGGCCGAGATA 900				
841 TACAACGTGGACAGCGGTGCTGACATGACCGGGTATCTTTACTGGCCGAGATA 900				

QY 361 AACCCGCAACCTTCTCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 420
 Db 361 AACCCGCAACCTTCTCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 420
 QY 421 GAAAGGAGGTGCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 480
 Db 421 GAAAGGAGGTGCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 480
 QY 481 GAGCCCTTAAAGATTTCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 540
 Db 481 GAGCCCTTAAAGATTTCTGACGAGCCGCTGCAACCAAGTCCAGAGCACTAG 540
 QY 541 TTGAGATGCAACCAAGTCCAGAGCCGCTGCAACCAAGTCCAGAGCACTAG 600
 Db 541 TTGAGATGCAACCAAGTCCAGAGCCGCTGCAACCAAGTCCAGAGCACTAG 600
 QY 601 GGTCTTGGAGGATGATGCTGCAACCAAGTCCAGAGCACTAG 660
 Db 601 GGTCTTGGAGGATGATGCTGCAACCAAGTCCAGAGCACTAG 660
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 Db 661 AAATCTGACAAAGAGGCTGCAACCAAGTCCAGAGCACTAG 720
 QY 721 GAAATCTTGAAGAGGCTGCAACCAAGTCCAGAGCACTAG 780
 Db 721 GAAATCTTGAAGAGGCTGCAACCAAGTCCAGAGCACTAG 780
 QY 781 AAGACCCATCTCTGCTGCAACCAAGTCCAGAGCACTAG 840
 Db 781 AAGACCCATCTCTGCTGCAACCAAGTCCAGAGCACTAG 840
 QY 841 TACAACTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 900
 Db 841 TACAACTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 900
 QY 901 GCTCTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 960
 Db 901 GCTCTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 960
 QY 961 AATGCTCTTCTGATGACCTGCAACCAAGTCCAGAGCACTAG 1020
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 QY 1021 ATGAGGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1080
 Db 1021 ATGAGGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1080
 QY 1081 ATCTTAATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1140
 Db 1081 ATCTTAATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1140
 QY 1141 ATTATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1200
 Db 1141 ATTATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1200
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 QY 1261 GAGGATCTGACAAAGGCTGCAACCAAGTCCAGAGCACTAG 1320
 Db 1261 GAGGATCTGACAAAGGCTGCAACCAAGTCCAGAGCACTAG 1320
 QY 1321 AGCAGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1380
 Db 1321 AGCAGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1380
 QY 1381 CGCTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1440
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 QY 1441 AAAACATGCTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1500

Db 1441 AAAGACATGCTGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1500
 QY 1501 GATTAAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1560
 Db 1501 GATTAAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1560
 QY 1561 ATTATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1620
 Db 1561 ATTATGAGGAGGCTGCAACCAAGTCCAGAGCACTAG 1620
 QY 1621 GAGGATCTGACAAAGGCTGCAACCAAGTCCAGAGCACTAG 1680
 Db 1621 GAGGATCTGACAAAGGCTGCAACCAAGTCCAGAGCACTAG 1680
 RESULT 11
 AAS06702
 ID AAS06702 standard; cDNA, 1662 BP.
 XX
 AC AAS06702;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #2.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN M0200138503-42.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000MO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGEN) SUGEN INC.
 XX
 PI Plozman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 DR WPI; 2001-343950/36.
 DR P-PSDB; AAU03502.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 PS Example 1; Fig 1; 433pp; English.
 XX
 CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. influenza),
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX

Query Match	99.6%;	Score 1652.6;	DB 4;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1655; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

QY	1	ATGSGAGCAATGAGGGGGCCCTGAGCAACCTGATGCGCAACACCGCTTACCTGCAAGCCCGG	60
Db	1	ATGSGAGCAATGAGGGGGCCCTGAGCAACCTGATGCGCAACACCGCTTACCTGCAAGCCCGG	60
QY	61	AAGCCCTCGAGACTGAGCAGCAAGAAGCTGAGAGGGGGGGGGCGGCTGACCTTGGCCCTGCCC	120
Db	61	AAGCCCTCGAGACTGAGCAGCAAGAAGCTGAGAGGGGGGGGGCGGCTGACCTTGGCCCTGCCC	120
QY	121	GGGCTGCAAGGACTGCGCGGAGCTCGCGCAGAGGTGCTCCCTGAACCTTTCACAGCCCTGTGT	180
Db	121	GGGCTGCAAGGACTGCGCGGAGCTCGCGCAGAGGTGCTCCCTGAACCTTTCACAGCCCTGTGT	180
QY	181	GAGCAGCAGGCCCATGAGTGGGCGCGCCCTTCCCTGGAATTCTTCGAGCAAGTGGCCAGGTTC	240
Db	181	GAGCAGCAGGCCCATGAGTGGGCGCGCCCTTCCCTGGAATTCTTCGAGCAAGTGGCCAGGTTC	240
QY	241	CGCAAGCGGCAACCTTCTTAGAGACGTGCAAACTGAGAGCTGCGCGAGGAGAGAGACCC	300
Db	241	CGCAAGCGGCAACCTTCTTAGAGAGCTGCAAACTGAGAGCTGCGCGAGGAGAGAGACCC	300
QY	301	ACCAAGACAGGGGCGCTGCAAGGGGCTGGTGGCACTTGTGGAGTGGCCCTGCCCCGGGG	360
Db	301	ACCAAGACAGGGGCGCTGCAAGGGGCTGGTGGCACTTGTGGAGTGGCCCTGCCCCGGGG	360
QY	361	AACCCGCAACCTTCTCAGACGAGCGGTGGGACACAGATGCGCAACAGCCACACACTGAG	420
Db	361	AACCCGCAACCTTCTCAGACGAGCGGTGGGACACAGATGCGCAACAGCCACACACTGAG	420
QY	421	GAGAGCGAGTGGCTGCAATGACGTGCGCAAGGCTGAGGCGCAATGCTTTCTTGCAGAG	480
Db	421	GAGAGCGAGTGGCTGCAATGACGTGCGCAAGGCTGAGGCGCAATGCTTTCTTGCAGAG	480
QY	481	CAGCCCTTAAAGATTTCCGTGACAGGGCCCTTCAACACAGTTTCTGCAGTGAAATTC	540
Db	481	CAGCCCTTAAAGATTTCCGTGACAGGGCCCTTCAACACAGTTTCTGCAGTGAAATTC	540
QY	541	TTTGAGATGCAACAGATGTCAGACAAATGTACTTCACTGAGTTCAAGTCTGGGAAAGGT	600
Db	541	TTTGAGATGCAACAGATGTCAGACAAATGTACTTCACTGAGTTCAAGTCTGGGAAAGGT	600
QY	601	GTTTTGGGGAGGTATGTGCTCCAGAGTGAATAAACTGGAGAGATGATGCTGTAAAG	660
Db	601	GTTTTGGGGAGGTATGTGCTCCAGAGTGAATAAACTGGAGAGATGATGCTGTAAAG	660
QY	661	AAATGSAACAAGAGCGGAGCTGAAGAAAGAGGTGGCGAGAGATGGCTCTCTTGGAAAG	720
Db	661	AAATGSAACAAGAGCGGAGCTGAAGAAAGAGGTGGCGAGAGATGGCTCTCTTGGAAAG	720
QY	721	GAAATCTTGGAGAAAGGTACAGACCCTTTCATTTGTCTCTCTGAGCTATGCTTGAAGAC	780
Db	721	GAAATCTTGGAGAAAGGTACAGACCCTTTCATTTGTCTCTCTGAGCTATGCTTGAAGAC	780
QY	781	AAACCCCATCTCTGCTTGTCTATGAGCTTGAATGAGAGATGGGAGAGACCTTCAAGTTCACATC	840
Db	781	AAACCCCATCTCTGCTTGTCTATGAGCTTGAATGAGAGATGGGAGAGACCTTCAAGTTCACATC	840
QY	841	TACAACTGGGCAACGGTGGCTGAGCACTGAGACCGGGGTATCTTTTACTGGGCCCAAGATA	900
Db	841	TACAACTGGGCAACGGTGGCTGAGCACTGAGACCGGGGTATCTTTTACTGGGCCCAAGATA	900
QY	901	GGCTGTGGAGTGTGCACTCTCATGAACTTGAGCATGTCTATGTGGACATGAAGCTTAG	960
Db	901	GGCTGTGGAGTGTGCACTCTCATGAACTTGAGCATGTCTATGTGGACATGAAGCTTAG	960
QY	961	AATGTGCTTGTGATGACCTCGGCAACTGCAAGTTATCTGACCTGAGGCGGCGCTGTGAG	1020
Db	961	AATGTGCTTGTGATGACCTCGGCAACTGCAAGTTATCTGACCTGAGGCGGCGCTGTGAG	1020

Chr	Start (Mb)	End (Mb)	Gene	Transcript	Accession	Length (bp)	GC (%)	GC3 (%)	GC3+ (%)	GC4 (%)	GC4+ (%)	GC5 (%)	GC5+ (%)	GC6 (%)	GC6+ (%)	GC7 (%)	GC7+ (%)	GC8 (%)	GC8+ (%)	GC9 (%)	GC9+ (%)	GC10 (%)	GC10+ (%)	GC11 (%)	GC11+ (%)	GC12 (%)	GC12+ (%)	GC13 (%)	GC13+ (%)	GC14 (%)	GC14+ (%)	GC15 (%)	GC15+ (%)	GC16 (%)	GC16+ (%)	GC17 (%)	GC17+ (%)	GC18 (%)	GC18+ (%)	GC19 (%)	GC19+ (%)	GC20 (%)	GC20+ (%)	GC21 (%)	GC21+ (%)	GC22 (%)	GC22+ (%)	GC23 (%)	GC23+ (%)	GC24 (%)	GC24+ (%)	GC25 (%)	GC25+ (%)	GC26 (%)	GC26+ (%)	GC27 (%)	GC27+ (%)	GC28 (%)	GC28+ (%)	GC29 (%)	GC29+ (%)	GC30 (%)	GC30+ (%)	GC31 (%)	GC31+ (%)	GC32 (%)	GC32+ (%)	GC33 (%)	GC33+ (%)	GC34 (%)	GC34+ (%)	GC35 (%)	GC35+ (%)	GC36 (%)	GC36+ (%)	GC37 (%)	GC37+ (%)	GC38 (%)	GC38+ (%)	GC39 (%)	GC39+ (%)	GC40 (%)	GC40+ (%)	GC41 (%)	GC41+ (%)	GC42 (%)	GC42+ (%)	GC43 (%)	GC43+ (%)	GC44 (%)	GC44+ (%)	GC45 (%)	GC45+ (%)	GC46 (%)	GC46+ (%)	GC47 (%)	GC47+ (%)	GC48 (%)	GC48+ (%)	GC49 (%)	GC49+ (%)	GC50 (%)	GC50+ (%)	GC51 (%)	GC51+ (%)	GC52 (%)	GC52+ (%)	GC53 (%)	GC53+ (%)	GC54 (%)	GC54+ (%)	GC55 (%)	GC55+ (%)	GC56 (%)	GC56+ (%)	GC57 (%)	GC57+ (%)	GC58 (%)	GC58+ (%)	GC59 (%)	GC59+ (%)	GC60 (%)	GC60+ (%)	GC61 (%)	GC61+ (%)	GC62 (%)	GC62+ (%)	GC63 (%)	GC63+ (%)	GC64 (%)	GC64+ (%)	GC65 (%)	GC65+ (%)	GC66 (%)	GC66+ (%)	GC67 (%)	GC67+ (%)	GC68 (%)	GC68+ (%)	GC69 (%)	GC69+ (%)	GC70 (%)	GC70+ (%)	GC71 (%)	GC71+ (%)	GC72 (%)	GC72+ (%)	GC73 (%)	GC73+ (%)	GC74 (%)	GC74+ (%)	GC75 (%)	GC75+ (%)	GC76 (%)	GC76+ (%)	GC77 (%)	GC77+ (%)	GC78 (%)	GC78+ (%)	GC79 (%)	GC79+ (%)	GC80 (%)	GC80+ (%)	GC81 (%)	GC81+ (%)	GC82 (%)	GC82+ (%)	GC83 (%)	GC83+ (%)	GC84 (%)	GC84+ (%)	GC85 (%)	GC85+ (%)	GC86 (%)	GC86+ (%)	GC87 (%)	GC87+ (%)	GC88 (%)	GC88+ (%)	GC89 (%)	GC89+ (%)	GC90 (%)	GC90+ (%)	GC91 (%)	GC91+ (%)	GC92 (%)	GC92+ (%)	GC93 (%)	GC93+ (%)	GC94 (%)	GC94+ (%)	GC95 (%)	GC95+ (%)	GC96 (%)	GC96+ (%)	GC97 (%)	GC97+ (%)	GC98 (%)	GC98+ (%)	GC99 (%)	GC99+ (%)	GC100 (%)	GC100+ (%)	GC101 (%)	GC101+ (%)	GC102 (%)	GC102+ (%)	GC103 (%)	GC103+ (%)	GC104 (%)	GC104+ (%)	GC105 (%)	GC105+ (%)	GC106 (%)	GC106+ (%)	GC107 (%)	GC107+ (%)	GC108 (%)	GC108+ (%)	GC109 (%)	GC109+ (%)	GC110 (%)	GC110+ (%)	GC111 (%)	GC111+ (%)	GC112 (%)	GC112+ (%)	GC113 (%)	GC113+ (%)	GC114 (%)	GC114+ (%)	GC115 (%)	GC115+ (%)	GC116 (%)	GC116+ (%)	GC117 (%)	GC117+ (%)	GC118 (%)	GC118+ (%)	GC119 (%)	GC119+ (%)	GC120 (%)	GC120+ (%)	GC121 (%)	GC121+ (%)	GC122 (%)	GC122+ (%)	GC123 (%)	GC123+ (%)	GC124 (%)	GC124+ (%)	GC125 (%)	GC125+ (%)	GC126 (%)	GC126+ (%)	GC127 (%)	GC127+ (%)	GC128 (%)	GC128+ (%)	GC129 (%)	GC129+ (%)	GC130 (%)	GC130+ (%)	GC131 (%)	GC131+ (%)	GC132 (%)	GC132+ (%)	GC133 (%)	GC133+ (%)	GC134 (%)	GC134+ (%)	GC135 (%)	GC135+ (%)	GC136 (%)	GC136+ (%)	GC137 (%)	GC137+ (%)	GC138 (%)	GC138+ (%)	GC139 (%)	GC139+ (%)	GC140 (%)	GC140+ (%)	GC141 (%)	GC141+ (%)	GC142 (%)	GC142+ (%)	GC143 (%)	GC143+ (%)	GC144 (%)	GC144+ (%)	GC145 (%)	GC145+ (%)	GC146 (%)	GC146+ (%)	GC147 (%)	GC147+ (%)	GC148 (%)	GC148+ (%)	GC149 (%)	GC149+ (%)	GC150 (%)	GC150+ (%)	GC151 (%)	GC151+ (%)	GC152 (%)	GC152+ (%)	GC153 (%)	GC153+ (%)	GC154 (%)	GC154+ (%)	GC155 (%)	GC155+ (%)	GC156 (%)	GC156+ (%)	GC157 (%)	GC157+ (%)	GC158 (%)	GC158+ (%)	GC159 (%)	GC159+ (%)	GC160 (%)	GC160+ (%)	GC161 (%)	GC161+ (%)	GC162 (%)	GC162+ (%)	GC163 (%)	GC163+ (%)	GC164 (%)	GC164+ (%)	GC165 (%)	GC165+ (%)	GC166 (%)	GC166+ (%)	GC167 (%)	GC167+ (%)	GC168 (%)	GC168+ (%)	GC169 (%)	GC169+ (%)	GC170 (%)	GC170+ (%)	GC171 (%)	GC171+ (%)	GC172 (%)	GC172+ (%)	GC173 (%)	GC173+ (%)	GC174 (%)	GC174+ (%)	GC175 (%)	GC175+ (%)	GC176 (%)	GC176+ (%)	GC177 (%)	GC177+ (%)	GC178 (%)	GC178+ (%)	GC179 (%)	GC179+ (%)	GC180 (%)	GC180+ (%)	GC181 (%)	GC181+ (%)	GC182 (%)	GC182+ (%)	GC183 (%)	GC183+ (%)	GC184 (%)	GC184+ (%)	GC185 (%)	GC185+ (%)	GC186 (%)	GC186+ (%)	GC187 (%)	GC187+ (%)	GC188 (%)	GC188+ (%)	GC189 (%)	GC189+ (%)	GC190 (%)	GC190+ (%)	GC191 (%)	GC191+ (%)	GC192 (%)	GC192+ (%)	GC193 (%)	GC193+ (%)	GC194 (%)	GC194+ (%)	GC195 (%)	GC195+ (%)	GC196 (%)	GC196+ (%)	GC197 (%)	GC197+ (%)	GC198 (%)	GC198+ (%)	GC199 (%)	GC199+ (%)	GC200 (%)	GC200+ (%)	GC201 (%)	GC201+ (%)	GC202 (%)	GC202+ (%)	GC203 (%)	GC203+ (%)	GC204 (%)	GC2
-----	------------	----------	------	------------	-----------	-------------	--------	---------	----------	---------	----------	---------	----------	---------	----------	---------	----------	---------	----------	---------	----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	----------	-----------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	------------	-----------	-----

XX 06-MAR-2003.

PD 19-AUG-2002; 2002WO-EP009235.

XX 21-AUG-2001; 2001US-0313464P.

XX (PARR) BAYER AG.

XX XIAO Y;

DR WPI; 2003-278669/27.

XX P-PSDB; ABP96707.

XX New G-protein coupled receptor kinase polypeptides and polynucleotides,
XX useful in identifying modulators of the enzyme for treating cancer,
XX diabetes, a central nervous system disorder, a cardiovascular disorder or
XX asthma.

XX Claim 1; Fig 1; 129pp; English.

XX The present sequence encodes a human G protein-coupled receptor kinase
XX (GRK) protein (I). (I) has cytosolic, antidiabetic, neuroprotective,
XX nocrotic, cardiovascular, anti-Parkinsonian, cardiac, vasotropic and
XX antiasthmatic activities, and can be used in gene therapy. (I) can be
XX regulated to treat cancer, diabetes, a central nervous system (CNS)
XX disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
XX Parkinson's disease), cardiovascular disorders (e.g. congestive heart
XX failure, myocardial infarction, ischemic diseases of the heart or
XX hypertensive vascular disease), asthma and chronic obstructive pulmonary
XX disorder (COPD). GRK molecules are useful in screening for agents that
XX regulate or decrease the activity of a GRK. GRK sequences may also be used
XX for detecting diseases and abnormalities or susceptibility to diseases
XX and abnormalities related to the presence of mutations in the nucleic
XX acid sequences that encode the GRK enzyme

XX Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

XX Query Match 99.6%; Score 1652.6; DB 7; Length 1662;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 1655; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 60
DB 1 ATGTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 60
QY 61 AAGGCTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 120
DB 61 AAGGCTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 120
QY 121 GGGCTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 180
DB 121 GGGCTGTGACATGGGGGCTCTGACAACTGATCGCCCAACCGCTACTGAGAGGCGGG 180
QY 181 GAGGACACCCATGATGTCGCGCTCTTCCGTGACACTTCCGTGACACTTCCGTGACACTT 240
DB 181 GAGGACACCCATGATGTCGCGCTCTTCCGTGACACTTCCGTGACACTTCCGTGACACTT 240
QY 181 GAGGACACCCATGATGTCGCGCTCTTCCGTGACACTTCCGTGACACTTCCGTGACACTT 240
DB 181 GAGGACACCCATGATGTCGCGCTCTTCCGTGACACTTCCGTGACACTTCCGTGACACTT 240
QY 241 CGAAGAGCGGCACTTCTTAGAGAGCTGACAACTGAGAGCTGAGAGCTGAGAGCTGAGAG 300
DB 241 CGAAGAGCGGCACTTCTTAGAGAGCTGACAACTGAGAGCTGAGAGCTGAGAGCTGAGAG 300
QY 301 ACCAAGAGAGCGGCTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 360
DB 301 ACCAAGAGAGCGGCTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 360
QY 361 AACCCGCAACCTTCTTCTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
DB 361 AACCCGCAACCTTCTTCTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 420
QY 421 GAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480
DB 421 GAAGAGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 480

QY 481 CAGCCCTTAAAGATTTCTGACCAAGCCCTTCTGACCAAGATTTCTGACCAAGATTTCTGAC 540
DB 481 CAGCCCTTAAAGATTTCTGACCAAGCCCTTCTGACCAAGATTTCTGACCAAGATTTCTGAC 540
QY 541 TTGAGATGCAACCAAGTGTGACAACTGATCTGATCTGATCTGATCTGATCTGATCTGAT 600
DB 541 TTGAGATGCAACCAAGTGTGACAACTGATCTGATCTGATCTGATCTGATCTGATCTGAT 600
QY 601 GGTGTTGGGAGGATATGTCGCTGACAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAG 660
DB 601 GGTGTTGGGAGGATATGTCGCTGACAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAG 660
QY 661 AAATGCAAGAGAGCGGCTGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAG 720
DB 661 AAATGCAAGAGAGCGGCTGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAG 720
QY 721 GAAATCTTGAAGAGTGTGACAGAGGCTTCTGATCTGATCTGATCTGATCTGATCTGATCT 780
DB 721 GAAATCTTGAAGAGTGTGACAGAGGCTTCTGATCTGATCTGATCTGATCTGATCTGATCT 780
QY 781 AAGAGCCATCTGCTGCTGATGACAGGCTGATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 840
DB 781 AAGAGCCATCTGCTGCTGATGACAGGCTGATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 840
QY 841 TACAGGTGAGAGCGGCTGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAG 900
DB 841 TACAGGTGAGAGCGGCTGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAG 900
QY 901 GCGTGTGAGATGCTGACATCTGATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 960
DB 901 GCGTGTGAGATGCTGACATCTGATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 960
QY 961 AATGTGCTTGTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1020
DB 961 AATGTGCTTGTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1020
QY 1021 ATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1080
DB 1021 ATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1080
QY 1081 ATCTTAATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1140
DB 1081 ATCTTAATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1140
QY 1141 ATTTAATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1200
DB 1141 ATTTAATGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1200
QY 1201 GAGGATCTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1260
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 AC ABZ56934;
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 DT 04-APR-2003 (first entry)
 XX
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 KW Human; RGSNO9; heart disease; cancer; omentopathy; gene; ds.
 XX
 OS Homo sapiens.
 XX
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 FT /*tag= a
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 PN MO2002103020-A1.
 XX
 PD 27-DEC-2002.
 XX
 PF 14-JUN-2002; 2002MO-JP005942.
 XX
 PR 15-JUN-2001; 2001JP-00182654.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Koyama N, Tanida S, Yamamoto K;
 XX
 DR WPI; 2003-157045/15.
 DR P-PSDB; ABP60078.
 XX
 PT Novel disease-associated gene of the RGS gene family and its product,
 PT applicable in diagnosis of and screening for drugs for heart diseases,
 PT cancers and omentopathy.
 XX
 BS Claim 6; Page 81-82; 96pp; Japanese.
 XX
 CC The invention relates to a novel disease associated gene and its uses.
 CC The gene and its encoded protein are useful for diagnosis of and
 CC screening for drugs for heart diseases, cancers and omentopathy. The
 CC current sequence represents the human RGSNO9 encoding DNA sequence
 XX
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 Query Match 71.6%; Score 1187.8; DB 7; Length 1191;
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 DB 1081 ATCTTAATGAAAGGTAAGTATCTTATCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1140
 QY 1141 ATTATGAAATGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1191
 DB 1141 ATTATGAAATGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1191
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 ID AAD46351 standard; cDNA; 1486 BP.
 XX
 AC AAD46351;

WELL; 2001-5/08/2/64.
P-PSDB: AAG77816

541 TTGGAGATGCAACCCAGTGTGAGACAACTTCACTTGAGCTTACGAGTGCCTCCCAATCCCT 600

THE UNIVERSITY OF CHICAGO

```
OY 601 GGTGTTGGGAGGTATGTCGTCAGGTGAAAAACACTGGAGAGATGATGCTGTAG 660
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    |||
OY 661 AAATGGAACAAGAGGCTGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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    |||
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    |||
OY 781 AAGACCATCTCTGCTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	398.6	24.0	2978	AK051405	AK051405 Mus muscu
2	375	22.6	2989	11 BC057206	BC057206 Mus muscu
3	311.8	18.8	1201	13 BX404586	BX404586 BX404586
4	311.6	18.8	2329	11 BC027597	BC027597 Homo sapi

C	5	307	18.5	917	13	BX392018
	6	304.6	18.4	1721	29	AY406080
	7	300.2	18.1	1058	13	BQ057469
	8	299.2	18.0	1019	13	BQ061148
	9	295	17.8	1721	29	AY406082
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	13	272.2	16.4	601	12	BM674749
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	21	265.4	16.0	998	13	BQ057613
	22	264.8	16.0	1032	12	BM472080
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	24	264.2	15.9	851	13	BQ230423
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	28	258	15.6	713	10	AM173009
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ALIGNMENTS

RESULT 1	AK051405	2978 bp	mRNA	linear	HTC 20-SRP-2003
LOCUS	AK051405				
DEFINITION	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone: D130046K22 product: g PROTEIN-COUPLED RECEPTOR KINASE GPR6 (EC 2.7.1.1) homolog [Mus musculus], full insert sequence.				
ACCESSION	AK051405				
VERSION	AK051405.1	GI:26094516			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
REFERENCE	99279253				
PUBMED	10349636				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
REFERENCE	20499374				

**PUBMED
REFERENCE
AUTHORS**

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Shibata, K., Itoh, M., Aizawa, K., Nagakita, S., Sasaki, N., Carninci, P., Komio, H., Akiyama, Y., Nishi, K., Kitamurai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Fujimoto, R., Matsunouchi, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yamaguchi, S., Inoue, K., Togawa, Y., Iwano, E., Ohara, E., Watanahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y., 2000. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexillary sequencer. *Genome Res.* 10(11), 1757-1771 (2000).

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

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RESULT 2
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 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
 1 (bases 1 to 2989)
 Strusberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences

TITLE
 JOURNAL MEDLINE
 PUBMED 22388257
 1247932
 2 (bases 1 to 2989)
 AUTHORS Strausberg, R.
 DIRECT SUBMISSION
 JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgabs-remail.nih.gov
 Tissue Procurement: Leihar Hennighausen Ph.D., Priscilla Futh
 Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhi.nih.gov
 Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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FEATURES

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 Db 929 GTGCTGTGATGATGATGATGAGGAGACCTCAAGTTCCATCTACACCTGAG 988
 Qy 852 CAGCGGTGCTGACATGAGCGGCTATCTTTTCTGCGCCAGATGACCTGAGAT 911
 Db 989 CAGCGGTGCTTCTGATGACAGTGTGCTTCTTCTGATGCTGATGCTGCTGCT 1048
 Qy 912 GCTGACCTTCCATGAACTGCGCATGCTCTATCGGACATGAAAGCTGAGATCTTCT 971
 Db 1049 GGAAGCTGACCGGAGACGATGTGTGATGAGGATCTAAAGCCAGAGAAATCTTCT 1108
 Qy 972 GATGACCTGCAATCTGAGTTTCTGACCTGAGGCTGCGCTGAGATGAGGCTG 1031
 Db 1109 GATGACCTGCAATCTGAGTTTCTGACCTGAGGCTGCGCTGAGATGAGGCTG 1168
 Qy 1032 CAAGCCATCAACCAAGGCTGAGCAACAGGTTATAGGCTCTGATGATCTTGA 1091
 Db 1169 CCAAGCATCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1226
 Qy 1092 AAAGGTAATGTTCTATCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1151
 Db 1227 -AATGAGCTGACAGTTCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1285
 Qy 1152 GATGACCTGCAATCTGAGTTTCTGACCTGAGGCTGCGCTGAGATGAGGCTG 1211
 Db 1286 GATGACCTGCAATCTGAGTTTCTGACCTGAGGCTGCGCTGAGATGAGGCTG 1345
 Qy 1212 GCAGAAATCTGCAAGAGGCTGAAATCTCAAGATGATGATGATGATGATGAT 1271
 Db 1346 GCGGCTGCTGCAAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1405
 Qy 1272 AGATTTTGCAGGCTCTTCTTGTGTAAGAAACAGAGCAACGTTTGAAGCAAGAAA 1331
 Db 1406 ACTGTGTTCTCAGCTTCTTGAAGAGACCTGCTGAGAGGCTGAGAGGCTG 1465
 Qy 1332 GTCTGATGATCCCAAGAAACATCAATTTCTTTAAACATCAATTTCTTCTGAGAG 1391
 Db 1466 CGCCGCTGAGTAAAGAGCAACCTTTTCAAGAACTGAATTTCAAGCGCTGAGAG 1525
 Qy 1392 TGCGCTTAAAGAACCCCATTTGTCAGACCTTCAAGTGTGATGATGATGATGAT 1451
 Db 1526 TGCGATGCTGAGGCACTTTTAAGCTGATCCAGGCTATTTATGAGAGATGCT 1585
 Qy 1452 TGAATTTGATGATTTCTGAGGTTGCGGCTGAGATTTGATGATGATGATGATGAT 1511
 Db 1586 GGAATTTGAGAGTTCTTCAAGTTTGAAGTGTGATGATGATGATGATGATGAT 1645

Qy 1512 CTTCAAAAACCTTTCGACAGGCTGCTTCTTATGATGACGAGAAATTTAAGAAC 1571
 Db 1646 CTACAGAGATTTCCACAGGCTGATGATGATGATGATGATGATGATGATGAT 1705
 Qy 1572 GGAAGCTTTGAGAGACTGAATGAC 1596
 Db 1706 CAGAGCTTTCAGAGACTCAATGTC 1730

RESULT 3

BX404586/c 1201 bp mRNA linear EST 13-MAY-2003
 LOCUS BX404586 Homo sapiens NEUROBLASTOMA

DEFINITION BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 CS0DA004YM05 3-PRIME, mRNA sequence.

ACCESSION

BX404586
 EST.

KEYWORDS

BX404586.1 GI:30648023

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 1201)

AUTHORS

Li, W. B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

FEATURES

Location/Qualifiers

source

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DA004YM05"

/tissue_type="NEUROBLASTOMA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched

double-strand cDNA was digested with NotI and cloned into

the NotI and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

ORIGIN

Query Match 18.8%; Score 311.8; DB 13; Length 1201;

Best Local Similarity 59.8%; Pred. No. 3.5e-60;

Matches 539; Conservative 1; Mismatches 358; Indels 3; Gaps 1;

Qy 522 GTTTCGAGTGAAGAACTCTGAGATGCAACAGGTGCAAGATCTTCACTGATGTT 581

Db 1004 KTTCTGAGAGGAAATGAGCTGAAAGCAGGCTGACCAAAACCTTGAACAAATA 945

Qy 582 CAGAGTGTGAGGAAAGTGTGTTGGGAGGATGTGCGCTGCAAGTGAACACTGG 641

Db 944 CGAGTCTCTGGGAAAGTGTGTTGGGAGGATGTGCGCTGCAAGTGTGCGGCAACG 885

Qy 642 GAAGATGTATGCTTGAAGAACTGCAAGAGGCGCTGAAAGAAAGGTGGGAGAA 701

Db 884 TAAGATGTATGCTTGAAGAACTGCAAGAGGCGCTGAAAGAAAGGTGGGAGAA 825

Qy 702 GATGCTCTCTGGAAGAAATCTTGAAGAGTCAAGACCTTTCAATGCTCTCT 761

Db 824 CATGCGCTGAAAGCAAGATCTTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 765

QY 762 GGCCTATGCTTTGAGAGCAAGCCATCTGCTGCTGATGAGTGGGG 821
 Db 764 GGCTATGCTTTGAGAGCAAGCCATCTGCTGCTGATGAGTGGGG 705
 QY 822 AGACCTCAAGTTCCACATCTTCAACAGTGGGACCGTGGCTGSACTAGAGCGGGAT 881
 Db 704 GCACTCAAGTTCCACATCTTCAACAGTGGGACCGTGGCTGSACTAGAGCGGGAT 645
 QY 882 CTTTATCTGGCCCAAGTATGCTGGGATGCTGACCTTCATGAACTGGGATCTCTA 941
 Db 644 CTTTATCTGGCCCAAGTATGCTGGGATGCTGACCTTCATGAACTGGGATCTCTA 585
 QY 942 TCGGACATGAAAGCTGAGATGCTGCTGATGATGCTGCACTGCACTGATATCTGA 1001
 Db 584 CAGGACCTGAAAGCTGAGATGCTGCTGATGATGCTGCACTGCACTGATATCTGA 525
 QY 1002 CTTGGGCTGGCCCTGAGATGCAAGGCTGGCAAGCCATCACCAAGGCGTGGAACTGA 1061
 Db 524 CTTGGGCTGGCCCTGAGATGCAAGGCTGGCAAGCCATCACCAAGGCGTGGAACTGA 465
 QY 1062 TGGTATCATGCTCTCTGATGCTTATGAAAGATTAATTCCTATCTGCTGAGATG 1121
 Db 464 GGGTATCATGCTCTCTGATGCTTATGAAAGATTAATTCCTATCTGCTGAGATG 408
 QY 1122 GTTGGCAATGGGATGAGATTTATGAAATGTTGCTGAGCAACATCTCAAGATTA 1181
 Db 407 GTGGGCTCTGCTGCTCTCTGATGATGATGAGGCTGAGGCTCTTCCAGAGAG 348
 QY 1182 CAAGGAAAGTCAAGTAAAGGATCTGAAAGAAAGATCTGCAAGAGTCAAAAT 1241
 Db 347 GAAAGAAAGTCAAGTAAAGGATCTGAAAGAAAGATCTGCAAGAGTCAAAAT 288
 QY 1242 CCAAGATATTAATCTTCAAGAGAAAGAAAGATTTTCAAGCTCTTCTTGGCTAAGA 1301
 Db 287 TTCCAGAGGCTTTTCCCGAGGCTGCTCACTTCTCAAGCTCTCTTCAAGAGAG 228
 QY 1302 ACCAGAGCAAGCTTGAAGAGCAAGAAAGTGTATGATCCCAAGAAATCATTTCT 1361
 Db 227 TCCGAGAGGCTTGGGCTGCTGAGGAGGCTGAGGCTGAGAGAGAGAGAGAGAGAG 168
 QY 1362 TAAAGCATCACTTCTCTGCTGAGAGGCTGAGGCTTAAATGAAAGAGAGAGAGAG 1421
 Db 167 TAAAGCATCACTTCTCTGCTGAGAGGCTGAGGCTTAAATGAAAGAGAGAGAGAG 108
 QY 1422 C 1422
 Db 107 C 107

RESULT 4
 BC027597 2329 bp mRNA linear HTC 01-MAY-2002
 LOCUS Homo sapiens, similar to G protein-coupled receptor kinase 2-like
 DEFINITION (Drosophila), clone IMAGE:4830673, mRNA.
 ACCESSION BC027597 GI:20379554
 VERSION 1
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2329)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki

Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systembiology.org>
 contact: amadan@systembiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Ketterman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 34 Row: 1 Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4885346
 This clone has the following problem: frame shifted.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4830673"
 /issue_type="Testis"
 /clone_lib="NIH MGC 97"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

ORIGIN
 Query Match 18.8%; Score 311.6; DB 11; Length 2329;
 Best Local Similarity 57.4%; Pred. No. 5,5e-60;
 Matches 623; Conservative 0; Mismatches 454; Indels 9; Gaps 3;

QY 477 AGAGCAAGCCCTTAAAGATTCGTCAGCAAGGCTTCTACAGAAAGTTCTGCAAGTGA 536
 Db 921 AGGAGAACCATTTGAAGAAATACCAAGAAAGTCAATTTTCTGATTTTACATGAA 980
 QY 537 ACTCTTGAGATGACACCAAGTGTCAAGCAAGTCTCACTGATTTCAAGTGTGGGAA 596
 Db 981 ATGGCTGAAAGACCAACCGTAAACAAAGACATTTAGACATTAAGAGTTCTAGAAA 1040
 QY 597 AGGTGTTTTGGGAGGATATGCTGCTCAAGTGAAGAAACCTGGAAAGATATGCTG 656
 Db 1041 AGCGGATTTGAGAGGTTTCCGCTGTCAGAGTGCAGAGCAAGAAATATATGCTG 1100
 QY 657 TAAAGAACTGCAAGAAAGCGCTGAAGAAAGTGGGAGAGAGTGTCTCTTGA 716
 Db 1101 CAAAAGCTCAAAAAGAAATTAAGAGAGAAAGGTAAGCTATGCTTAATGA 1160
 QY 717 AAGGAATCTTGAAGAGTCAAGAGCCCTTCAATGCTCTCTGAGCTTATGCTTGA 776
 Db 1161 GAAAAGATTTCTGAGAAAGTGAAGATGATGATGATGATGATGATGATGATGATG 1220
 QY 777 GAGCAAGACCATCTCTGCTTGTCAATGAGCTGATGAATGGGAGAGCTCAAGTTCA 836
 Db 1221 AACCAAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280
 QY 837 CATCTCAAGCTGGGCAAGGCTGAGCTGAGATGAGCGGAGATCTTATCTGAGCCCA 896
 Db 1281 CATTTAGAACTGGGCAATCCCGCTTGTATGAGCAAGAGCGGTTTCTATGCTGAGA 1340
 QY 897 GATAGCTTGGGAGTGTGACATTCATGAACTGCGATGCTTATCGGAGCATGAAGCC 956
 Db 1341 GCTGTGTTGGGCTTGGAGATTTACAGAGGAAAGAAATGATACAGAGCTTGAAGCC 1400
 QY 957 TGAAGATGCTTCTGATGAGCACTGAGCACTGAGATATCTGACTGGGCTGGCGCT 1016
 Db 1401 TGAAGATATTTCTGATGATGAGCACTGAGCACTGAGATATCTGACTGGGCTGGCG 1460
 QY 1017 GAGATGAGAGGCTGAGCAAGCCATCAAGAGGCTGAGCAAGATGATGATGATGATG 1076
 Db 1461 AGAGATCCCAAGAGAGAGAGGCTTCAAGAGAGAGATGAGAGAGAGCTTCAAGAGCC 1520
 QY 1077 TGAAGTCTTATGAAAGATGATTAATTCCTATCTGAGATGATGATGATGATGATG 1136
 Db 1521 TGAAGTGTCA--ATTAATGAAAGATATACGTTAGTCCGATTTGTGGGAGCTTGGCTG 1577

QY 1137 CAGCATTTTGAATGGTGTGTCAGCAACACCATTTCAAGATTACAGAGAAAGCTCAG 1196
 DB 1578 TGTATCTTATGAAATGATTCAGGAGCATCTCCATTTCAAAAATACAGAAAGATGCTCA 1637
 QY 1197 TAAAGAGATCTGAGCAAGACCTGCAAGACGATGCAAAATCCACATGATTAATT 1256
 DB 1638 ATGGAGAGAGTGTGATCAAGAA--TCAAGAAATGATACGAGAGATATTTCTGAGAGTT 1694
 QY 1257 CACAGAGAGCAAAAGATATTTGCAAGCTCTTCTTGCTAGAAACCAAGCAACGCTT 1316
 DB 1695 TTGAGAGATGCCAAATCTATCTGAGATGTTACTCAACAGAAATCAAGCAACGCTT 1754
 QY 1317 AGAAGACAGAGAAAG--TGTGATGATCCAGAGAAACATATTTCTTTAAACATGAA 1373
 DB 1755 GGGCTGCAGGGGCGAGGAGCGCTGGGGTGAAGACCAACCCCTGTTCAAGACATGAA 1814
 QY 1374 CTTTCTGCTGGAAGCTGCTTAATTTGAACCCCAATTTGTCAGACACCTTCAGTGT 1433
 DB 1815 CTTTCAGAGGCTGAGAGCAAAACATGCTGAGAGCCCTTCTGCTCTGATCTTCATGCT 1874
 QY 1434 TTATGCCAAGACATGCTGAAATTTGATTTCTCTGAGTTGCGGGGGTGAATTTGA 1493
 DB 1875 TTACTGTAAAGCTCTGATGATGAGCAAGTTCTGCGGGTGAAGAGATCTACCTGGA 1934
 QY 1494 TCAAGATGAGCAAGTTCTTCAAAAACCTTTGCGAGAGTGTCTTCTTACGATGCA 1553
 DB 1935 CACCCAGATGAGCAATCTATGCTGCTGCTGCTACCGGGTGTCTTCATCTCCCTGGA 1994
 QY 1554 GAGAGA 1559
 DB 1995 GAATGA 2000

RESULT 5
 BX32018/c 917 bp mRNA linear EST 13-MAY-2003
 LOCUS BX32018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 DEFINITION Homo sapiens cDNA CSODL010YD11 3-PRIME, mRNA sequence.
 ACCESSION BX32018
 KEYWORDS BX32018.1 GI:30607809
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 917)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSOBAL046ZH12_CS04416_1&cluster=3090.f.
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Parady Avenue Genoscope Sequence ID: CSOBAL046ZH12_CS04416_1.
 Location/Qualifiers
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 location=Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="CSODL010YD11"
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 /cell_line="RAMOS CELL LINE"
 /clone_id="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)

ORIGIN

primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 18.5%; Score 307; DB 13; Length 917;
 Best Local Similarity 63.8%; Pred. No. 3,7e-59;
 Matches 482; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

QY 459 GGGCATGCTTTCTTGCAGAGAGACCTTTAAGGATTTGGACACAGCCCTTACAGA 518
 DB 796 GACCCAGAGTACTGAGCTGAGCTGCCCTTTTGCAGTCTCCAGACATCTTACTCA 737
 QY 519 CAAATTTGCGAGTGAAGAACTTTGAGATCAACAGTGTCAACAAATTTCACTGA 578
 DB 736 CCGTTTCTGAGTGTGAAGTGTGTAAGGACCGAGTGAACAAACACCTTCAGGCA 677
 QY 579 GTTCAGAGTGTGAGAGAGTGTGTTGGGAGGTATGTGCTGCTCCAGGTGAAAAACAC 638
 DB 676 ATACGAGTCTGGGCAAAAGTGTGAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 617
 QY 639 TGGAGATGATATGCTGTAAAGAACTGGAACAGACCGCTGAAGAGAAAGTGTGCA 698
 DB 616 AGGTAAAGATATGCTGTGCAAGAGCTGAGAAAGACGATCAAGAGCGGAGGGA 557
 QY 699 GAAGATGCTCTCTTGGAAAGGAAATCTTGGAGAGTGTGAGAGCTTCAATGCTTC 758
 DB 556 GGCATATGAGCTGAAGAGAGAGATCTGAGAGAAAGTGAACAGATTTGTATGAGAG 497
 QY 759 TCTGCTTATGCTCTTGTAGAGCAAGACCAATCTGCTGCTGTATGAGAGCTGATGAT 818
 DB 496 CTTGGCTTACGCTTATGAGACCAAGAGACCGCTGTGCTGTGCTGTGCTGTGCTGTGCT 437
 QY 819 GGGAGACCTCAAGTTCACATCTACAGAGTGTGAGACCGCTGTGCTGTGCTGTGCTGTGCT 878
 DB 436 GAGGACCTCAAGTTCACATCTACAGAGTGTGAGACCGCTGTGCTGTGCTGTGCTGTGCT 377
 QY 879 GATCTTTTACTGAGCCAGATGAGTGTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 938
 DB 376 CGTCTTCAAGCGCGCGAGATCTGTGCTGTGAGAGTGTGAGTGTGAGTGTGAGTGT 317
 QY 939 CTATCGGACATGAAAGCTGAGAAATGTCTTGTGAGTGTGAGTGTGAGTGTGAGTGT 998
 DB 316 GTACAGGACCTGAAAGCCGAGAAACATCTTGTGTGATGACAGGSCACATCCGATCTC 257
 QY 999 TGACCTGAGGCTGAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1058
 DB 256 TGACCTGAGGCTGAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 197
 QY 1059 CAATGCTTACATGCTCTCTGAGATCTTAATGAAAGGTAAGTATTCTTATCTGTGGA 1118
 DB 196 CGTGGTTACATGCTCTCGGAG--GTGCTGAAGATGAAAGGTTACACCTTCAGCCCTGA 140
 QY 1119 CTGTTTGCATGAGATGAGATCTTATGAAATGTTCTGAGCAACATCAAGA 1178
 DB 139 CTGGTGGGCGCTGAGCTGCTCTGTAAGAGATGCAAGGCAAGTGTGCTTCCACAGA 80
 QY 1179 TTACAGAGAAAGTGTGATTAAGAGATCTGAGC 1213
 DB 79 GAGGAAAGAAAGATTAAGCGGAGAGGAGTGAAGC 45

RESULT 6
 AY406080 1721 bp DNA linear GSS 15-DEC-2003
 LOCUS AY406080
 DEFINITION Homo sapiens GPRK5 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY406080
 VERSION AY406080.1 GI:39762054
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1721)
 Mammalia: Eutheria: Primates: Catarrhini; Homidae; Homo.
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL
 Science 302 (5652), 1960-1963 (2003)

REFERENCE
 PUBMED
 14671302

AUTHORS
 2 (bases 1 to 1721)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /gene="GPRK5"
 /locus_tag="HCM2438"

ORIGIN

Query Match 18.4%; Score 304.6; DB 29; Length 1721;
 Best Local Similarity 49.5%; Pred. No. 1.9e-58;
 Matches 559; Conservative 0; Mismatches 561; Indels 9; Gaps 3;

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Oy 469 TTCTTGAAGAGCAGCCCTTTAGAGATTGCTGACAGCGCCCTTCTGACAAAGTTTGG 528
Db 402 TACCTGAGGGAGAACATTTCCAGCAATATCTGACAGATTTTGGACGCTTTCTC 461
Oy 529 CAGTGAACCTTTCAGATGCAACAGTGTGACACAAAGTCTTCACTGAGTTCAAGTG 588
Db 462 CAGTGAAGTGTGTAAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521
Oy 589 CTGGGAAAGGTGTTTGGAGGTATGTGCGCTTCAGGTGAAACATGTGGAAAGTG 648
Db 522 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 581
Oy 649 TATGCTGTATAAGAACTGACACAGAGCGGCTGAGAGAAAGGTGGCGAAGAGTGC 708
Db 582 TATGCTGTCAAGCGCTTGAAGAGAGAGAGATTAAGAAAGAGAGAGTCAATGCGC 641
Oy 709 CTCTTGAAGAAAGAAATCTTGAAGAGTCAAGAGCCCTTTCATTTCTCTGCGCTAT 768
Db 642 CTCAATGAGAGAGATCTCTGAGAGTCAAGATCAAGTTGTGTCAACCTGCGCTAT 701
Oy 769 GCTTTGAGAGCAAGCCCATCTGCTGCTTCAAGAGCTGATGATGAGTGGGAGACTTC 828
Db 702 GCTTCAAGACCAAGAGTCACTGTGCTGCTGCTGACATCAATGATGAGGAGTCACTG 761
Oy 829 AAGTTTCAATCTTACACAGTGGGACAGCTGAGCTGACATGAGCGGGGATCTTTAC 888
Db 762 AAGTTTCAATCTTACAAATGGGACACCTGCTGAGAGAGAGCGGCGCTTTGTTAT 821
Oy 889 TCGGCGAGATAGCTGTGGAGTCTGACATTCATGAACTCGGCAATCGTCTATGAGAC 948
Db 822 GCGGCGAGATCTCTGCGGCTTAGAAGACTTCACCGTAGAACACCGTCTACCGAGAT 881
Oy 949 ATGAAGCTGAGAAATGCTCTGAGATACCTCGGCACTGCAAGTTATCTGACCTGGG 1008
Db 882 CTGAAGCTTGAAGAAATCTCTGAGATATGAGTCAATGAGATCTCAAGACTGCGC 941
Oy 1009 CTGCGCGTGAAGTGAAGGATGAGCAAGCCATCAAGAGAGGCTGAGACCAATGTTAC 1068
Db 942 TTGCGCTGTAAGATCCCGAGGAGAGACTGATCCCGGCGGAGTGGGACCTGTGGCTAC 1001

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Oy 1069 ATGGCTCTGAGATCTTAATGAAAGTAAAGTAAATTTCTTACTCTGAGACTGTTTGGC 1128
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 Oy 1129 ATGGATGAGCAGATTTATGAATGTTGCTGAGCAACACCACTTCAAGATTAAGAGAA 1188
 Db 1059 CTGGCTGCTCATCTATGATGATGATGAGGCGCAGTGGCGCTTCCGCGCCGAGAGAG 1118
 Oy 1189 AAGTCACTAAGAGATCTGAAGCAAAAGTCTGCAAGAGTCAATTTCCAGCAT 1248
 Db 1119 AAGGTGAAGCGGAGAGAGTGAACCGCGGCTCTGAGAGAGAGAGGTATCTCCAC 1178
 Oy 1249 GATTAATCTCAAGAGAGAGCAAAAGTATTTGACAGCTCTTTGCTTGAAGACAGAG 1308
 Db 1179 ---AAGTTCTCGAGAGAGCCCAAGTCAATCTCAAGATGCTGCAAGAAATCGAAG 1235
 Oy 1309 CAAGCTTGAAG 1365
 Db 1236 CAGAGGCTGGGCTGCGCAG 1295
 Oy 1366 ACGATCAATCTTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1425
 Db 1236 AACATGAACCTTCAAGCTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1355
 Oy 1426 TCAGTGTATGCAAG 1485
 Db 1356 NNN 1415
 Oy 1486 GAATTTGATGACAAAGATAGCAGATTCTTCAAAAACCTTGCAGAGTGTCTCTATA 1545
 Db 1416 NNN 1475
 Oy 1546 GCATGACAG 1594
 Db 1476 NNN 1524

RESULT 7
 B0057469
 LOCUS
 DEFINITION
 AGENCOURT 6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
 5', mRNA sequence.
 ACCESSION
 B0057469
 VERSION
 B0057469.1 GI:19816809
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 (bases 1 to 1058)
 NIH-MGC <http://mgi.nci.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LINC2064 row: j column: 03
 High quality sequence stop: 631.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5813090"
 /tissue_type="T lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"

ORIGIN

/clone lib="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

Query Match 18.1%; Score 300.2; DB 13; Length 1058;
 Best Local Similarity 63.9%; Pred. No. 1.3e-57;
 Matches 471; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

459 GGCCATGCTCTTTCGAGACAGACCCCTTAAAGATTTCGACAGCCGCTTCTACGA 518
 5 GGACCCAGAGTACTAGAGCTGGCCCTTTTCCGCACTCTGACAGCATCTACTGAA 64
 519 CAAGTTCTGAGTGAAGAACTCTTGAGATGCAACAGTGTCAACAGTACTTCACTGA 578
 65 CGTTTCTGAGTGAAGTGGCTGAAAGGCGACAGTGAACAAAACCTTCAGGCA 124
 579 GTTCAGAGTCTGGGAGAAAGGTGTTTGGGGAGGTATGTGCTCCAGGTGAAAAAC 638
 125 ATACCGAGTCTGGGCAAGGTGGCTTTGGGAGGTGTGCTGCGAGGTGGGCGAC 184
 639 TGGGAAGATGATGCTCTGTAGAACTGACAAAGAGCGCTGAAGAAAGAGTGGCGA 698
 185 AGGTAAATGATGATGCTCTGCAAGAGCTGAGAAAAGCGGATCAAGAAAGGAAAGGGA 244
 699 GAAGATGAGCTCTTGGAAAGAAATTTTGGAGAGTGTGACAGCCCTTCACTTGTCTC 758
 245 GGCAATGGGGCTGAAGAGAAAGAGTCTGAGAAAGTGAACAGTATGTTATGTAG 304
 759 TCTGGCTTATGCTTTGAGAGCAAGACCATCTGCTTTCATGAGCCGTGATGATG 818
 305 CTGGGCTTACGCTTATGAGCAAGAGAGCGCTGTGCTGATGACATGATGAGCG 364
 819 GGGAGACCTCAAGTTCCACATCTACAGTGGGACGCTGGCTGACATGAGCGGCT 878
 365 GGGGACCTCAAGTTCCACATCTACAGTGGGACGCTGGCTTCCCGAGCGGCG 424
 879 GATCTTTTACCTGGCCCAATAGCTGTGGAGATCTGCACTCTCAATGAACTCGCATCT 938
 425 CGTCTTCTAGCGCCGAGATCTGCTGTGGCTGAGAGACCTGACCGGAGCGCATGCT 484
 939 CTATGGGACATGAAGCTGAGAAATGTGCTCTGATGACCTCGGCACTGAGATTATC 998
 485 GTACAGGAGCTGAAGCCGAGAAATCTTGCTGATGACAGGCGCATCTCGCATCTC 544
 999 TGAAGTGGGGCTGGCCGAGATGAGAAAGGTGGCAAGCCCATCAAGAGGCTGGAAC 1058
 545 TGACCTGGAGATAGTGTGATGTGCGAGGCGCAAGCATCAAGGCGCTGTGGCGAC 604
 1059 CAATGTATCATGCTCTCTGATGATCTTAATGAGAAAGTAAATCTCTTCTCTGGA 1118
 605 CGTGGGTATCATGCTCTCGAG--GTGGTGAAGAAATGAACGGTATACAGTCAAGCCCTTA 661
 1119 CTGGTTTGCATGGAGTGAAGCATTTATGAATGGTTGTGACGAAACCATTTCAAAG 1178
 662 CTGGTGGGGCTGGGCTGCTCTCTGTAGAGATGATGCAAGCATGCTGCTTCCAGCA 721
 1179 TTAAGAGAAAGTCA 1195
 722 GAGAGAGAGAGATCA 738

RESULT 8
 B0061148 1019 bp mRNA linear EST 02-APR-2002
 LOCUS B0061148
 DEFINITION AGNCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180

5', mRNA sequence.
 B0061148
 GI:19884933
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1019)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA library Preparation: Rubin laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: LLCM2083 row: h column: 05
 High quality sequence stop: 704.
 Location/Qualifiers

FEATURES

source

1..1019
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5920180"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 18.0%; Score 299.2; DB 13; Length 1019;
 Best Local Similarity 63.8%; Pred. No. 2.4e-57;
 Matches 470; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

459 GGCCATGCTTTTTCGAGACAGACCCCTTAAAGATTTCGACAGCCGCTTCTACGA 518
 5 GGACCCAGAGTACTAGAGCTGGCCCTTTTCCGCACTCTGACAGCATCTACTGAA 64
 519 CAAGTTCTGAGTGAAGAACTCTTGAGATGCAACAGTGTCAACAGTACTTCACTGA 578
 65 CGTTTCTGAGTGAAGTGGCTGAAAGGCGACAGTGAACAAAACCTTCAGGCA 124
 579 GTTCAGAGTCTGGGAGAAAGGTGTTTGGGAGATGTGCCCTCAAGTGAAGAAAC 638
 125 ATACCGAGTCTGGGCAAGGTGGCTTTGGGAGGTGTGCTGCGCAGGTGCGGCGAC 184
 639 TGGGAAGATGATGCTCTGTAGAACTGACAAAGAGCGCTGAAGAAAGAGTGGCGA 698
 185 AGGTAAATGATGATGCTCTGCAAGAGCTGAGAAAAGGAGATCAAGAAAGGAAAGGGA 244
 699 GAAGATGAGCTCTTGAAGAAAGAAATTTGAGAGTGTGACAGCCCTTCAATGTCTC 758
 245 GGCAATGGGGCTGAAGAGAGAGTCTGAGAAAGTGAAGAGTATGTTGTAGTGAAG 304
 759 TCTGGCTTATGCTTTGAGAGCAAGACCATCTGCTCTTGTATGAGCTGATGATGATG 818
 305 CTGGCTTACGCTTATGAGACCAAGAGAGCGCTGTGCTGCTGTGACATGATGAGCG 364
 819 GGGAGACCTCAAGTTCACATCTCAAGTGGGACGCTGGAGCATGAGCGCGCT 878

Query Match	17.8%	Score 295;	DB 29;	Length 1721;
Best Local Similarity	49.0%;	Pred. No. 3e-56;		
Matches 553;	Conservative 0;	Mismatches 567;	Indels 9;	Gaps 3

Dy
949 ATGACCTCAGGAATGTCGTTCGGATGACCTCCCGCAACTGCAGGTTATTCTGACCTGAGG 1008

Dy
882 CTAAAAACCGAAAACAATCTTGTGGATGATTATGGCCAAATAAGATCTCAGACCTCGGA 941

Dy
1009 CTCGCCGCTGAGAGATGAAGAAGGTGCGCAACCCTATACCAGAGGGCTGSAACCATGCTTAC 1066

Dd
942 CTCGCCGCTGAAGATCCCCGAGGAGAACCTTATTCGCTGCGGGTAGGCACTGTTGGCTCAC 1001

Dy
1069 AAGCTCTCTGAGATCCTAATGGAAGAGTAAGTTATTCCTATCTTGAGACTGCTTTGGCC 1128

Dd
1002 ATGGCCCCAGAAGTCTGAACAACBACGATATGACGTAGAGCCTTACTACTGG--GGC 1055

Dy
1129 ATGGAGATCGACATTTATGSAATGTTGCTCGACGAAACCCATTCAAAGATTCAAGSAA 1188

Dd
1059 CTGGGCTCTCTCATATATGATGATTGAAGCCAGTCAACATTTCCAGGTCGACAGAGAG 1148

Dy
1189 AAGGTCAGTAAAGAGATCTGAACGAAGAAGCTGCGAAGACAGAGGTCAATTTCCAGAT 1248

Dy
1119 AAGGTTAAGCGGGAAGAAGGTGGAATCCGCGGGTCTGAGACTGAG--AAGTATATTC 1175

Dy
1249 GATACCTTCACAAAGGAACAAAAGATTTTGAAGGCTCTTTGGCTAAGAAACCGAG 1308

Dd
1176 TCCAAGTCTCTTAAGAGGCCAATCCATCTGCAACATGCTGTCAACAAAGACTGAAG 1235

Dy
1309 CAACCTTAGAGAGCAGAGAAA---GTCTATATATCCGAGGAACATCATCTTCTTAA 1355

Dd
1236 CAGAGGCTGGGCTGCCAGAGAGAGGGGCCGCCAGGTCAAGAGCAACCTCTTCTTCAGG 1295

Dy
1366 AGCATCAACTTTCTCTCGCCTTGAAGCTGGCCCTAAATTGAACCCCATTTGTGTGACAGACCT 1425

Dd
1296 AACATGAACCTTTAAGGCGCTGAGAGCTGGAGATGTTGACCCCTCCCTCGTCCAGATNNN 1355

Dy
1426 TCAGTGGTTATGCCAAAGACATCGCTGAALLATGATTAATTCTCTGAGGTTCCGGGGGTG 1485

Dd
1356 NNN 1415

Dy
1486 GAATTATGACAAAGATATAGCAATTCTTCAAAAACCTTGCAGAGGTGCTTCTATA 1545

Dd
1416 NNN 1475

Dy
1546 GCATGCGAGGAAGAAATTATATGAACGGGACTGTTTGAGAACTGAATG 1594

ORGANISM	REFERENCE
<i>Homo sapiens</i>	Oh, K. N. S., Hahn, Y. Y., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. F., Cho, J. H., Cha, J. T., Cho, H. Y., Kim, T. W., Park, H. C., Yoo, J. S., and Kim, S. H. 1997.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (baes 1 to 560)

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

FEATURES

SOURCE

ORIGIN

Matches 37

[illegible]

243 *LMGGCAATAGAGCAACGAGACGGCGCTGTGCTGTGGCTGACACTGTATGTGAACGGGAGGAGCGAC* 300
 QY 826 *CTCAAGTTCCACATCTACACACGTG66CAGCGCTG66CCTGACATGTAGCGCGGTATCTTT* 885
 Db 301 *CTCAAGTTCCACATCTACACATGT66CAGCGCTG66CTTCCCGAAGCGG66CGCTTTTC* 360
 QY 886 *TACTG66CCGACATGTAGCTGTG66ATGTCTGACACCTCCATTAATGTG66CATGTGTATACG* 945
 Db 361 *TACGCGCGCGAGATCTGCTGTG66CTGTAGAGACCTGTGACCGGAGACGATGTGTATACG* 420

QY 946 GACATGAGCTGAGATGCTTCTGATGACCTCGGCACTGACGATTCATGACCTG 1005
 DB 421 GACCTGAGCCCGCAACATCTTGTGTATGACACAGCGCACATCCGCACTCTGACCTG 480
 QY 1006 GGGCTGGCCCTGAGATGAGAGGCTGCGAACCCATCACCCAGAGGCTGGAACCAATGCT 1065
 DB 481 GACATGAGCTGAGATGCTTGTGTATGACACAGCGCACATCCGCACTCTGACCTG 540
 QY 1066 TACATGAGCTGCTGATGAT 1082
 DB 541 TACATGAGCTGCGAGGT 557

RESULT 13
 BM697499 601 bp mRNA linear EST 28-FEB-2002
 LOCUS BM697499
 DEFINITION UI-E-DX0-agn-o-23-0-UI.r1 UI-E-DX0 Homo sapiens cDNA clone
 UI-E-DX0-agn-o-23-0-UI 5', mRNA sequence.
 BM697499
 ACCESSION BM697499.1 GI:19010757
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 601)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: benton-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 Seq primer: M13 Reverse.

FEATURES

source
 location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-DX0-agn-o-23-0-UI"
 /tissue_type="fetal eyes"
 /dev_stage="fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-DX0"
 /note="Organ. eye: Vector: pUT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-DX0 is a cDNA library containing the following tissue(s): fetal eyes. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pUT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is AGATCAGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 16.4%; Score 272.2; DB 12; Length 601;
 Best Local Similarity 67.5%; Pred. No. 2.7e-51;
 Matches 382; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 526 CTCAGTGGAAACTCTTCGATGCAACCACTGTCAAGAACTTCTGATGATG 585
 DB 1 CTCAGTGGAAAAGTGTGCGAAAGCGCAGCTGACAAAACCTTCAAGCAATCCGA 60
 QY 586 GTGCTGGGAAAAGCTGTTTGGGGAGGATGCGCTCCAGCAAAAAACATCGGGAAG 645
 DB 61 GTCTGGGAAAAGGCTGTTGGGGAGGATGCGCTCCAGCAAAAAAGGAGGAGTAA 120
 QY 646 ATGTATGCTGTAAAGAACTGGAACAAGCGCTGGAAGAAAGGTTGGCGAAGATG 705
 DB 121 ATGTATGCTGTAAAGAACTGGAACAAGCGGATCAAGAAAGGAGGAGGAGTAA 180
 QY 706 GCTCTCTGAAAAGAAATCTTGGAGAGTGCAGGCCCTTTCAATTGTCTCTGCGC 765
 DB 181 GCGCTGAAGAGAACAGATCTCGAGAAAGTGAACAGTGTGTGTAGTGAAGCTTGG 240
 QY 766 TATGCTTTGAGAGCAAGACCACTCTGCTTGTCAATGAGCCTGATGATGAGGAGAG 825
 DB 241 TATGCTTTGAGAGCAAGACCGCTGTGCTGTGCTGCTGATGATGAGGAGGAGAG 300
 QY 826 CTCAGTTCACATCTTACACAGTGGGCAAGCGTGGCTGAGCATGACCGGAGTAT 885
 DB 301 CTCAGTTCACATCTTACACAGTGGGCAAGCGTGGCTTCCCGAAGCGGAGCGTCTTC 360
 QY 886 TACTGCGCCCAATAGCTGTGGAGATCTGCAACCTCCATGAATGCGCATGTGTATCG 945
 DB 361 TACGCGCCCAATAGCTGTGGAGATCTGCAACCTCCATGAATGCGCATGTGTATCG 420
 QY 946 GACATGAGCTGAGATGCTTCTGATGACCTCGGCACTGCAAGTATTCGACCTG 1005
 DB 421 GACCTGAGCCCGCAACATCTTGTGTATGACACAGCGCACATCCGCACTCTGACCTG 480
 QY 1006 GGGCTGGCCCTGAGATGAGAGGCTGCGAACCCATCACCCAGAGGCTGGAACCAATGCT 1065
 DB 481 GACATGAGCTGAGATGCTTGTGTATGACACAGCGCACATCCGCACTCTGACCTG 540
 QY 1066 TACATGAGCTGCTGATGAT 1082
 DB 541 TACATGAGCTGCGAGGT 557

RESULT 14

B0061150 1017 bp mRNA linear EST 02-APR-2002
 LOCUS B0061150
 DEFINITION AGNCOURT_6862973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
 5', mRNA sequence.

ACCESSION B0061150
 VERSION B0061150.1 GI:19884936
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1017)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA library Preparation: Rubin Laboratory
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LICM083 row: h column: 07
 High quality sequence stop: 697.
 Location/Qualifiers

FEATURES

source

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1. 1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5920182"
/tissue_type="Lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the Laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

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Query Match      16.4%; Score 272.2; DB 13; Length 1017;
Best Local Similarity 58.8%; Pred. No. 3.7e-51;
Matches 526; Conservative 0; Mismatches 359; Indels 9; Gaps 3;

QY 704 TGGCTCTCTGGAAGAAATCTTGAGAGGTCAGACCCCTTTCATTTGCTCTG 763
DB 1 TGGCCCTCATGAGAGAGAGATCTCGAGAGGTCAACGATGATGTTGTTCACTGG 60
QY 764 CCTATGCTTTGAGAGAGAGACCCATCTTCTGCTTCATGAGCCTGATGAATGGGAG 823
DB 61 CCTATGCTTCAGAGAGAGAGATGACGTGTGTTGCTTCTGACATGATGAGGAGT 120
QY 824 ACCCTGAATTCACATCTTCAACCGGGGACGGTGGCTGACAGTGGCGGTGATCT 883
DB 121 ACTGAGATTCACATCTTCAACCGGGGACCGTGGCTTGAAGAGAGCGGCTTGT 180
QY 884 TTACTCGGCCAGATAGCTGTGGAGTGTGACCTCCATGAACTGGAGTCGTATC 943
DB 181 TTATAGGGGAGAGATCTCTGCGGCTTGAAGACCTCCACCGTGAACACCGTATCC 240
QY 944 GGAACATGAAGCTTGAGATGCTTCTTGATGACCTCGGACATGCGAGTTATGACC 1003
DB 241 GAGATCTGAAGCTTGAAACATCTGTTAGATGATTATGACATTAAGATCTGACCC 300
QY 1004 TGGGGCTGGCGTGAGAGAGAGTGGCAAGCCCATCAACAGAGGCTGGAACCAATG 1063
DB 301 TGGGCTGGCTGTGAAGATCCCGAGGAGACCTGATCCGCGCGCGGCTGAGCTGTG 360
QY 1064 GTTACATGCTCTCTGAGATCTTAATGAGAAAGTAAATTCTTCTGTCGACTGCT 1123
DB 361 GCTACATGCTCTGAGAGTCC--TGAACAACAGAGTACGCTGAGCCCTCACTACT 417
QY 1124 TTGCAATGAGATGACGATTTATGAATGGTGTGTCGACAGACCATTCGAAGTTACA 1183
DB 418 GGGGCTTGGCTGCTCATCTATGATGATGAGAGGCGAGTGGCGCTTCGCGGCGGCA 477
QY 1184 AGGAAAGGTGAGTAAAGAGATGTCGAACCAAGAACTCTGCAAGAGCTGAATTC 1243
DB 478 AGGAGAGGTGAGAGCGGAGAGGTGACCGCGGCTCTGAGAGCGAGG---AGTGTG 534
QY 1244 AGCATGATACTTCACAGAGAGCAAAAGATATTGTCAGGCTCTTCTTGCTGAAGAAC 1303
DB 535 ACTCCCAAGATTCTCGAGAGAGCCAGATCATCTGCAAGATGCTGCTCAAGAAAGATG 594
QY 1304 CAGAGCAAGCTTAAAGAGAGAGAAA--GTCTGATGATCCCAAGAGAAATCATTTCT 1360
DB 595 CAGAGCAAGCTTAAAGAGAGAGAAA--GTCTGATGATCCCAAGAGAAATCATTTCT 654
QY 1361 TTAAGAGATCACTTCTGCTGAGAGAGTGGCTTAATGAATCCCATTTTGTGCAAG 1420
DB 655 TCGAGAACTGAATCTTAAGAGCTTGAAGCGGAGATGTTGAGCCCTCTCTTCACAG 714
QY 1421 ACCCTTCAGTGTATTAGCCAAAGACATGCTGAATGATTTCTCTGAGGTTCCGAG 1480

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DB 715 ACCCCGCGCTGTGACTGTAAAGAGTGTGACATGACAGATTCTCACTGTTAG 774
QY 1481 GGGTGAATTTATGACAAATATGACATTTTCAAAAACTTGGACAGTGTCTTC 1540
DB 775 GCGCAATCTGACACACAGACAGACACTTCTTATCTCAAGTTCTCCAGGGCTCTGTGT 834
QY 1541 CTATAGATGCGAGAGAAATTAATGAAAGGAGCTGTTGAGAGACATGANTG 1594
DB 835 CCATCCCATGTCACACAGATGATGAAACAGATGCTTAAAGAGCTGAACG 888

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RESULT 15
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wtd17a07.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE:228372.3, similar to gb:U15388 G PROTEIN-COUPLED RECEPTOR
KINASE GRK5 (HUMAN); mRNA sequence.
A1934968
EST.
A1934968.1 GI:5673838

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: c9apbs-remail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1030 Std Error: 0.00
Seq primer: -40UP from 51bco
High quality sequence stop: 483.
Location/Qualifiers
1. 815

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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_id="Soares NFL T GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

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ORIGIN

```

Query Match      16.3%; Score 270.6; DB 9; Length 815;
Best Local Similarity 62.3%; Pred. No. 7.5e-51;
Matches 439; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

QY 469 TTCTTGAAGAGAGCGCTTTAAGATTTGTCACACGCGCTTCAACAAATTTCTG 528
DB 711 TACTTGAAGAGAGAGCGCTTTAAGATTTGTCACACGCGCTTCAACAAATTTCTG 652
QY 529 CAGTGAAGCTCTTCAAGATGCAACAGTGTGACAAGTACTTCACTGAGTTCAGAGTG 588
DB 651 CAGTGAAGTGTGTGAAGAGCAACCGGTGACCAAAACATTTCAAGAGATGTGAGTGG 592
QY 589 CTGGGGAAGAGTGTGTGTGGGAGATGTGTGCGCTCAAGGTGAAGAAACATCGGAAGATG 648
DB 591 CTAGGAAAGAGGCGCTTCGGGTAGGTCTGTGCTGCTCAGGTTGCGGCGCACGGGTANATG 532

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QY 361 AACCCGCAACCTCTCTCTCAAGCCGCTGCGCAACCAAGTCCCAAGCACTGAG 420
DB 714 AACCCGCAACCTCTCTCTCAAGCCGCTGCGCAACCAAGTCCCAAGCACTGAG 773
QY 421 GAAAGCGAGTGTCTGAGTCACTGCGCAAGGCTGAGGCACTGCTTTTGGAAAG 480
DB 774 GAAAGCGAGTGTCTGAGTCACTGCGCAAGGCTGAGGCACTGCTTTTGGAAAG 833
QY 481 CAGCCCTTAAAGATTCTGACAGCGCTTCTCAAGCAAGTTTCTGAGTGAATCT 540
DB 834 CAGCCCTTAAAGATTCTGACAGCGCTTCTCAAGCAAGTTTCTGAGTGAATCT 893
QY 541 TTTCAGATGACCAAGTGTCAAGCAAGTCTCAAGTCTCAAGTCTGAGTGAAG 600
DB 894 TTTCAGATGACCAAGTGTCAAGCAAGTCTCAAGTCTCAAGTCTGAGTGAAG 953
QY 601 GGTCTTGGGAGGTATGCTGCTGAGTGAAGCACTGAGGAGATGATGCTGTAG 660
DB 954 GGTCTTGGGAGGTATGCTGCTGAGTGAAGCACTGAGGAGATGATGCTGTAG 1013
QY 661 AAATGGAACAAGAGCGCTGAGAGAAAGTGTGAGAGATGCTGCTTGAAG 720
DB 1014 AAATGGAACAAGAGCGCTGAGAGAAAGTGTGAGAGATGCTGCTTGAAG 1073
QY 721 GAAATCTTGAAGAGTGTGAGAGCGCTTCTGCTGCTGCTGCTGCTGAGC 780
DB 1074 GAAATCTTGAAGAGTGTGAGAGCGCTTCTGCTGCTGCTGCTGCTGAGC 1133
QY 781 AAGATCCATCT 840
DB 1134 AAGATCCATCT 1193
QY 841 TACAAGTGTGAGCGCTGAGCACTGAGCACTGAGCGAGTATCTTTTCTGAGC 900
DB 1194 TACAAGTGTGAGCGCTGAGCACTGAGCACTGAGCGAGTATCTTTTCTGAGC 1253
QY 901 GCCTGTGAGTGTGAGCACTGAGCACTGAGCGAGTATCTTTTCTGAGC 960
DB 1254 GCCTGTGAGTGTGAGCACTGAGCACTGAGCGAGTATCTTTTCTGAGC 1313
QY 961 AATGTCTTCTGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1020
DB 1314 AATGTCTTCTGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1373
QY 1021 ATGAAGGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1080
DB 1374 ATGAAGGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1433
QY 1081 ATCTTAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1140
DB 1434 ATCTTAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1493
QY 1141 ATTTAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1200
DB 1494 ATTTAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1553
QY 1201 GAGGATCTGAGCAAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1260
DB 1554 GAGGATCTGAGCAAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1613
QY 1261 GAGGATCTGAGCAAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1320
DB 1614 GAGGATCTGAGCAAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 1673
QY 1321 AGCAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1380
DB 1674 AGCAAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1733
QY 1381 CGCTGTGAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1440
DB 1734 CGCTGTGAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 1793

QY 1441 AAGACATGCTGAATTTGATGATTTCTCTGAGTGTGAGGAGTGTGAATTTGATGACAA 1500
DB 1794 AAGACATGCTGAATTTGATGATTTCTCTGAGTGTGAGGAGTGTGAATTTGATGACAA 1853
QY 1501 GATPAGCACTTCTTCAAAAATTGAGAGTGTCTTCTGATGATGAGCAAGAA 1560
DB 1854 GATPAGCACTTCTTCAAAAATTGAGAGTGTCTTCTGATGATGAGCAAGAA 1913
QY 1561 ATTATGAAACGGAGCTGTTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1620
DB 1914 ATTATGAAACGGAGCTGTTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1973
QY 1621 GAGGTATTTATCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1659
DB 1974 GAGGTATTTATCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2012

RESULT 2
US-09-802-117-1
Sequence 1, Application US/09802117
Patent No. 644456
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilgowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polymu
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 60/198,449
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1662
TYPE: DNA
ORGANISM: homo sapiens
US-09-802-117-1

Query Match 99.8%; Score 1655.4; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 60
DB 1 ATGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 60
QY 61 AAGCCTCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 120
DB 61 AAGCCTCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 120
QY 121 GGGCTGTGAGGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 180
DB 121 GGGCTGTGAGGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 180
QY 181 GAGGAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 240
DB 181 GAGGAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 240
QY 241 GAGGAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 300
DB 241 GAGGAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 300
QY 301 ACCAAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 360
DB 301 ACCAAGCAAGCGATCTGAGTGTGAGCACTGAGCGAGTGTGAGCACTGAGCGAGTATCTTTTCTGAGC 360
QY 361 AACCCGCAACCTCTCTCTCAAGCCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 420
DB 361 AACCCGCAACCTCTCTCTCAAGCCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 420
QY 421 GAAAGCGAGTGTGAGCGCTGAGCACTGAGCGAGTATCTTTTCTGAGC 480

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Db 421 GAGAGGAGTGGCTGGACGAGTGGAGGCTGAGGCTGCTTCTTGCAAGAG 480
Qy 481 CAGCCCTTTAAGGATTTCTGACCAAGGCTTCTAAGCAAGTTCTGCAAGTAACTC 540
Db 481 CAGCCCTTTAAGGATTTCTGACCAAGGCTTCTAAGCAAGTTCTGCAAGTAACTC 540
Qy 541 TTGCAATGTCACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAGTGTGAC 600
Db 541 TTGCAATGTCACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAGTGTGAC 600
Qy 601 GGTGTTGGGAGGATGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 601 GGTGTTGGGAGGATGTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 661 AAATGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 661 AAATGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Qy 721 GAAATCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 GAAATCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy 781 AAGACCATCTCTGCTTGTATGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 AAGACCATCTCTGCTTGTATGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 841 TACACGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 TACACGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy 901 GCTGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 901 GCTGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy 961 AATGTTCTTCTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 AATGTTCTTCTGAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy 1021 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1021 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Qy 1081 ATCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 ATCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Qy 1141 ATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Db 1141 ATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
Qy 1201 GAGGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Db 1201 GAGGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
Qy 1261 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1261 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Qy 1321 AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 1321 AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Qy 1381 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db 1381 CGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Qy 1441 AAAAGCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Db 1441 AAAAGCATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
Qy 1501 GATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1501 GATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
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Db 1501 GATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Qy 1561 ATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
Db 1561 ATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
Qy 1621 GAGGATATTCATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
Db 1621 GAGGATATTCATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680

RESULT 3
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 631423
; GENERAL INFORMATION:
; APPLICANT: GIBBS, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1
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Query Match 99.7%; Score 1654.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGTTGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db 1 ATGTTGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Qy 61 AAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 61 AAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Qy 121 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 121 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 181 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 181 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy 241 CGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 241 CGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Qy 301 ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 AACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 AACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 421 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 481 CAGCCCTTTAAGGATTTCTGACCAAGGCTTCTAAGCAAGTTCTGCAAGTAACTC 540
Db 481 CAGCCCTTTAAGGATTTCTGACCAAGGCTTCTAAGCAAGTTCTGCAAGTAACTC 540
Qy 541 TTGCAATGTCACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAG 600
Db 541 TTGCAATGTCACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAGTGTGACCAAG 600
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Db 2316 CGAAGGGGGGACCTCTAGAGGACGTGACAGACTGGGACCTGGCCGAGGAGGACCC 2375
 QY 301 ACCAAAGACAGCGGCTGCAAGGAGCTGGTGGCCACTTTGGAGAGGCCCTGGCCCGGAG 360
 Db 2376 ACCAAGACAGCGGCTGCAAGGAGCTGGTGGCCACTTTGGAGAGGCCCTGGCCCGGAG 2435
 QY 361 AACCGCAACCCCTTCTCAGCGAGGCGCTGGCCACCAAGTGGCAAGGACCACTGAG 420
 Db 2436 AACCGCAACCCCTTCTCAGCGAGGCGCTGGCCACCAAGTGGCAAGGACCACTGAG 2495
 QY 421 GAAGAGCAGTGGCTGCAAGTGCCTGGCCAGGCTGAGGCCATGGCTTTCTTGGCAAG 480
 Db 2496 GAAGAGCAGTGGCTGCAAGTGCCTGGCCAGGCTGAGGCCATGGCTTTCTTGGCAAG 2555
 QY 481 CAGCCCTTAAAGATTTCGAGCAGGCGCTTACAGCAAGTTTCTGAGTGAAGAACGC 540
 Db 2556 CAGCCCTTAAAGATTTCGAGCAGGCGCTTACAGCAAGTTTCTGAGTGAAGAACGC 2615
 QY 541 TTGAGATGCAACCAAGTGCAGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGT 600
 Db 2616 TTGAGATGCAACCAAGTGCAGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGT 2675
 QY 601 GGTTTGGGAGGTATGTGCTCCAGGTGAAAAACACTGGGAAGATGTAT 651
 Db 2676 GGTTTGGGAGGTATGTGCTCCAGGTGAAAAACACTGGGAAGATGTAT 2726

RESULT 8

US-08-464-954A-2
 ; Sequence 2, Application US/08464954A
 ; Patent No. 6255069

GENERAL INFORMATION:

APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,

APPLICANT: PRIYA

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSER: Jane Massey Licata, Esq.

STREET: Woodland Falls Corporate Park

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,954A

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076,084

FILING DATE: June 11, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: JEFF-0118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2848

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

ANTI-SENSE: NO

US-08-464-954A-2

Query Match

25.3%; Score 419.8; DB 3; Length 2848;

Best Local Similarity 56.2%; Pred. No. 4.8e-94;

Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

QY 15 GGCCCTGAGCAACTGATTCGCAACACCGCTTACCTGCAAGCCCGAAGCCCTGCACTG 74
 Db 65 GGAAGCTGAGCAACTGATTCGCAACACCGCTTACCTGCAAGCCCGAAGCCCTGCACTG 124
 QY 75 CGAGCAAG---AGCTGCAAGCGCGCGGTGTAAGCTTGACCTGCGGCGTCAAGG 131
 Db 125 AAATCGAAAGGCAAAAGCAAAATGCGGAGATGCTCAAGTTCCCTCAATCAAGCA 184
 QY 132 CTGGCGAGAGCTCCGCCAAGAGCTGCTCCCTGAACCTTCAAGAGCTGTGAGCAGCAGCC 191
 Db 185 GTGCGAAGAGCTGCGGCTGAGCTTCAAGCTGATCAAGCTGTGTGCGAGCGGACCG 244
 QY 192 CATGCTGCGGCTCTTCCGTGACTTCTTACCAAGTCCCAAGTCCGATTCGCAAGCGGCG 251
 Db 245 CATGCGGCGCTGCTGTTCGAGAGTTCTGTGCCAAGAGCGCGAGCTGAGCCGCTGCGT 304
 QY 252 AACCTTCTAGAGAGCTGCAAGACTGGAGCTGGCCGAGAGAGGACCAACAAGACG 311
 Db 305 CGCCTTCTGATGAGGAGTGGCCGAGATGAGTGAACCCGGAATGACAGCGAAAGCGATG 364
 QY 312 CGGCTGCAAGGAGCTGTGGCCACTTGTGCGAGTGCCTGCGCGGAGAACCCGCAACC 371
 Db 365 TGAGCGGCAAG---TACGCAAGATTTTGTAGCCCAACGAGGCTCTGACCTTCACTCCTGA 421
 QY 372 CTTCCTGACCAAGGCGCTGTGGCCACCAAGTGCACCACTGAGAGAGAGAGCAAGT 431
 Db 422 GGTCCCGCGGAGCTGTGTGAGAAC--TGCAACCGCGGCTGAGCAGGCTCCCTGCAAG 480
 QY 432 GGTGCAAGTGAAGCTGCGCAAGCTGAGGCGCAATGGCTTTTTCGAAGAGCAGCCCTTAA 491
 Db 481 ACCTTTTCAGAGACTACCCGCGCTA--CCGAGAGTACTTGAAGCGTGGCCCTTTTGC 538
 QY 492 GGAATTCGTGACCAAGCGCTTCTACACCAAGTTCTGCAAGTGAAGAACTTTCGAGATGCA 551
 Db 539 GGAATTCGTGACCAAGCGCTTCTACACCAAGTTCTGCAAGTGAAGAACTTTCGAGATGCA 598
 QY 552 ACCAGTGTGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGTGTTTGGGGA 611
 Db 599 GCGAGTGTGACCAAGTACTTCACTGAGTTCAGAGTCTGGGAAAGGTGTTTGGGGA 658
 QY 612 GGTATGTGCGCTGCGGTGAAAGAACTGAGGAAGTATGCTGTAGAGAACTGAGCA 671
 Db 659 GGTATGTGCGCTGCGGTGAAAGAACTGAGGAAGTATGCTGTAGAGAACTGAGCA 718
 QY 718 GAAAGTGAACAGTATGTTGATGAGCTTGGCTTACGCTTACAGCAAGAGCGGCT 791
 Db 778 GAAAGTGAACAGTATGTTGATGAGCTTGGCTTACGCTTACAGCAAGAGCGGCT 838
 QY 792 CTGCTTGTGATGAGCTTGAATGAGGAGAGACCTGAATCTCAATCTCAACGCGG 851
 Db 839 GTGCTGTGCTGACACTGATGAAAGCGGAGCACTCAAGTTCACATCTCAACATGAG 898
 QY 852 CACCGGTGCTGACATGAGCGGAGTGAATCTTAACTCGGCGCAAGATAGCTGTGGAT 911
 Db 899 CCAAGCTGCTTCCCGAAGCGGAGCGGCTCTTCAAGCGCGGAGATGTGCTGAGCT 958
 QY 912 GCTGACTTCTGATGAATCGGCAATGCTTATGCGGAGCAATGAAGCTGAGAAATGCTTCT 971
 Db 959 GAAAGCTGTGACACCGGAGCGCAATCGTGTACAGGACCTGAACCCGAGAACATCTTGCT 1018
 QY 972 GGAATGACCTGCGCAACTGAGGTTATCTGACCTGGGCGTGGCGTGAAGTGAAGGAGTGG 1031
 Db 1019 GGAATGACCTGCGCAACTGAGGTTATCTGACCTGGGCGTGGCGTGAAGTGAAGGAGTGG 1078

Db 747 GAAAGTGAACAGAGGAGTTGATGAGCTGGCTACGCTATAGACCAAGAGCGCT 806
 Qy 792 CTGGCTTGTATGAGCTGATGAAATGGGGGAGACCTGAAGTTCCATCACTCAAGCTGG 851
 Db 807 GTGGCTGTGCTGACCTGATGAAGGGGGGAGACCTGAAGTTCCATCACTCAAGCTGG 866
 Qy 852 CAGCGTGGCTGAGATGAGCCGGGTGATCTTTTATCTGGCCGATGAGCTGTGGAT 911
 Db 867 CAGGCTGTGCTTCCCGAAGCGCGGGCCGCTTTATAGCCCGAGATCTGGCTGTGGCT 926
 Qy 912 GCTGACCTTCATGAACCTGGGATGCTTATGCGGACATGAAGCTTGAAGATGCTTCT 971
 Db 927 GGAGGACCTGACCGGAGACCGATGCTGACAGGACCTGAAAGCCGAGAACTTCTCT 966
 Qy 972 GGATGACCTGCGCACTGAGGTTATCTGACCTGGGGGCGGCGCTGAGATGAAGGGG 1031
 Db 987 GGATGACCAAGCCACATCGCATCTGACCTGAGGAGTACCTGTGCACTGTGCCGAGGG 1046
 Qy 1032 CAGGCCATCAACCCAGAGGGCTGGAACCAATGTTATCTGAGCTCTGATCTTATGGA 1091
 Db 1047 CAGACCATCAAGGGGCGGTGTGGGACCGTGGTTTACATGGCTCCGAG---GTGGTAA 1103
 Qy 1092 AAGGTAAATTATCTCTATCTGTGACCTGTTGCTGATGAGATGCAATTTATGAAT 1151
 Db 1104 GAATGAACGGTACACCTTCAAGCCCTGACGTGTGGGGCTCGCTCTCTGTACAGAT 1163
 Qy 1152 GGTGTGGGAGCAACCATTCATCAAGATTTCAAGGAAAGGTCAAGTAAAGGATCTGAA 1211
 Db 1164 GATGCGAGGCGCATGCTGCTTCCAGCAGAGAGAGAGAGATCAAGCGGAGAGGTGGA 1223
 Qy 1212 GCAGAGAACTCTGCAAGACAGAGCTCAATTCAGCATGATTAATTCACAGAGAGAA 1271
 Db 1224 GGGGCTGGTGAAGGAGGTCCCGAGAGATATCCAGAGCTTTTCCCGAGGCGGCTC 1283
 Qy 1272 AATATTTTGAAGCTCTTCTTGGCTAAGAAACAAGCAAGCTTGAAGAAAGAGAAA 1331
 Db 1284 ACTTTGCTCAGAGCTCTCTGCAAGAGACCTGCGAGACCTGGGGGTGTGTGGGGGAG 1343
 Qy 1332 GTCTGATGATCCAGAGAAACATCATTTCTTAAAGATCAATCTTCTGCGCTGGAGG 1391
 Db 1344 TGCCTCGAGGTGAAGAGACCCCTCTTTTAAAGAGTGAATCTCAAGCGGTGGAGC 1403
 Qy 1392 TGAGCTTAATGAACCCCATTTGTGCGAGACCTTCAAGTGTGTTATCCAAAGATGAGC 1451
 Db 1404 TGGCATGTGAGAGCGCGCTTCAAGCTGAGACCCCGAGCATTTACGCAAGAGATGCT 1463
 Qy 1452 TGAATGATGATTTCTTGAAGTTGCGGGGGTGAATTTGAATGAACAAGATTAAGAGTT 1511
 Db 1464 GACATTTGACATTTCTTCAAGCTGCAAGGGGTGAGCTGAGGCTTACCGACAGGACTT 1523
 Qy 1512 CTTCAAAACCTTGGCAGAGGCTGTTCCATAGATGAGGAGGAGAAATTAAGAAAC 1571
 Db 1524 CTACAGAGATTTGCGCAGAGGAGTGTGCCATCTCCCTGAGAGAAAGATGTGAGAC 1583
 Qy 1572 GGGACTGTTGAGGAATGAATGAC 1596
 Db 1584 CGAGTGTCTTCCAGAGCTGATGTC 1608

RESULT 10 US-08-454-439-12

; Sequence 12, Application US/08454439
 ; Patent No. 5591618

GENERAL INFORMATION:

; APPLICANT: Chanlry, David
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Hoeksra, Merle F.
 ; TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
 ; TITLE OF INVENTION: Kinase GRK6
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,439
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/221,817
 ; FILING DATE: 31-MAR-1994
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NO. 5591618and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31981
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELETYPE: 25-3856
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2204 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 31..1758
 ; US-08-454-439-12

Query Match 25.2%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 1.1e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

Qy 15 GGCCTGGAACAATCGATCGCAACAACGCTTACCTGAGAGCCCGGAGCCCTGAGCTG 74
 Db 33 GAGCTCGAGACATCTGAGAGACAGGTGCTACTCAAGGCTCCGAGAAAGGTGGCGGTG 92
 Qy 75 CGACAGCAAG---AGCTGCAAGCGCGCGCGGTAGCGCTGACCTGCGCGGCTGCAAGG 131
 Db 93 AAATCCGAAGGCAAAAGCAAAAGAAATGGCGGAGATGCTCAAGTCTCTCAATCAACCA 152
 Qy 132 CTGGCGGAGCTCGCGCAAGAACTGCTCTGAATCTTCAAGCTGTGTGAGCAGAGCC 191
 Db 153 GTGGAGAGGCTCGCGCTCAAGCTCGAGGTGATCAAGCTGTGTGAGCGGCACTG 212
 Qy 192 CATCGGTGCGCGCTCTTCCGTGATCTTCTTGAAGCAAGTCCCAAGCTTCCGAGAGCGGC 251
 Db 213 CATTTGGCGCTGCTGTCTTCCGAGATTTCTGTGCCACAGAGCTGAGCTGAGCTGCTG 272
 Qy 252 AACCTTCTTGAAGACGTGCAAGAACTGGAGCTGGCGGAGGAGGAGCCCAAGAGCAG 311
 Db 273 CGCTTCTGATGAGGTGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATG 332
 Qy 312 CGGCTGCAAGGAGCTGTGAGCACTTGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTG 371
 Db 333 TGGCGGAGCG---TAAAGCAAGATTTTCTGAGCCACAGAGGCTTGAATCTTATCTG 389
 Qy 372 CTTCCTTACAGAGCGCGGTGCGCAAGTGGCAAGAGCAGCACTTGAAGAGAGAGAGT 431
 Db 390 GTTCCCGCGCAGCTGTGATGAGAC-TGACCCAGCGGCTGAGAGCAGGCTCCCTGCAAG 448

QY 432 GGCTGAGTGAAGCGCTGGCGAAGGCTGAGGCGCATGGCTTTCTTGAAGAGAGCCCTTAA 491
 DB 449 ACCTTTTCAGGAAGTCAACCGGCTGA--CCCAAGATACCTGAGCGTGGCCCTTTTTC 506
 QY 492 GAATTTCTGTAACAGCGCTTCTACACAGATTTCTGCAAGTGAATCTTCAGATGCA 551
 DB 507 CGACTACCTCCAGCAGCATCTACTTCAACGTTTCTCAGTGGAAAGTGGCTGGAAGGCA 566
 QY 552 ACCAGTCCAGCAAGATCTTCACTGAGTTCAGAGTGTCTGGGAAAGTGGTTTGGGGA 611
 DB 567 GCGAGTGAACAAAAACCTTTCAGCAATACCGATCTGGGTAAAGTGGCTTTGGGA 626
 QY 612 GGTATGCGCGTCCAGGTGTAAGAAACATGGGAATGTATGCTGTAAAGAACTGACAA 671
 DB 627 GGTGCGCTGCGCAAGGTGCGGCGCCAGGTAATGTATGCTGTAAAGAAAGCTAAGAA 686
 QY 672 GAAGCGCTGAAGAAAGAGTGGCGAAGATGCTCTTGGAAAGAAATCTTGA 731
 DB 687 AAGCGATCAAGAAAGCGAAGGAGGAGCCATGCGCTGAACGAAAGCAGATCTTGA 746
 QY 732 GAAGTCCAGAGCCCTTCACTTGTCTCTGCGCAATGCTTGAAGCAAGCCATCT 791
 DB 747 GAAGTGAACAGTATGTTGTATGATGCTTGGCTTACGCTTATGAGCAAGAGCGCT 806
 QY 792 CTGCTTGTCTAGAGCTGATGATATGGGAGAGCTTCAAGTTCACATCTCAACCTGAG 851
 DB 807 GTGCTGTGTGCTGACATGATGATGAGGGGAGAGCTTCAAGTTCACATCTCAACCTGAG 866
 QY 852 CAGCGTGGCTGGAAGTGAAGCGGAGTATTTTACTGCGCCAGATAGCTGTGGAT 911
 DB 867 CAGGCTGGCTTCCCGAAGCGGAGCGCTTCTACGCGCGAGATGCTGTGGCT 926
 QY 912 GCTGCACTTCCATGAATCTGCGCATGCTTATCGGAGATGAGAGCTGAGATGCTTCT 971
 DB 927 GAGAGACTGACCGGAGGAGATGATGATGAGGAGCTGAAAGCCGGAACATCTTGT 986
 QY 972 GATGACTCTGCGCAACTGAGGTATCTGACTTGGGCTGCGCGTGAAGTGAAGGAGT 1031
 DB 987 GATGATCAAGGCGCAATCGCATCTCTGAGCTGAGATGAGCTGTGATGCTGCCAGAG 1046
 QY 1032 CAAGCCATCAACCCAGAGGCTGGAACCAATGTTTCAATGCTCTGAGATCTTAATGA 1091
 DB 1047 CCAAGCATCAAGAGGAGTGGGAGCCGTTGATGCTGCGGAG--GTGGTGA 1103
 QY 1092 AAGGTAACTTATCTTATCTGTGAGTGTGTTGGCAAGGATGAGCAATTTAATAAT 1151
 DB 1104 GAATGAGCGTACAGTTTACGCTGAGCTGTGGGAGTGTGCTCTCTGATGAGAT 1163
 QY 1152 GATGCTGAGCAAGCAACCATTAAGATTAAGAGAAAGTCAAGTAAAGGATCTGA 1211
 DB 1164 GATCGAGGCGAGTGGCTTCTCAAGAGAGAAAGATCAAGGAGGAGAGGTGA 1223
 QY 1212 GCAAGAACTCTGCAAGAGAGTCAATTCAGCATGATTAATCTTCAAGAGAGCAAA 1271
 DB 1224 GCGGCTGTGAAGAGGTCCCGAGAGTATTCAGGCGCTTTCGCCGAGGCCGCTC 1283
 QY 1272 AATATTTGAGAGCTCTTCTGCTAAGAAACAGAGCAAGCTTAAGAAAGCAAGAAA 1331
 DB 1284 ACTTGTCTCAAGCTCTCTCTGCAAGAGCCCTGCGAAGCCCTGGGGTGTGTGGGGGAG 1343
 QY 1332 GTCTGATGATCCAGAGAAATCATTTCTTAAAGATCAATCTTCTGCTGAGAGC 1391
 DB 1344 TGCCGCGAGGTGAAGAGAGACCCCTCTTTTAAAGAGTGAATCTTCAAGGCGTGGAGC 1403
 QY 1392 TGCCCTAATTAACCCCATTTGTGCGAGACCTTCAAGTGTATTAAGCAAGAGATGCG 1451
 DB 1404 TGCAATGCTGAGCGCGCTTCAAGCTGAGCCCGCAATTAATGCAAGAGATTTCT 1463
 QY 1452 TGAATGATGATTTCTGAGGTTTGGGGGGTGAATTTGATGCAAAAGATTAAGAGAT 1511
 DB 1464 GGAATTTGAAGATTTCTTACGTTAAGGGGTGAGAGCTTGAAGCTTCAAGAGAGATCT 1533
 QY 1512 CTTCAAAATTTTGCAGAGGTGCTTCTTATGATGAGGAGAGAAATTAAGAAAC 1571

DB 1524 CTACAGAAATTTTGGCAAGGCAAGTGTCCATCCCTTGGAGAGAGAGATGTGGAGAC 1583
 QY 1572 GGGACTGTTGAGAACTGAATGAC 1596
 DB 1584 CGAGTCTTCAAGAGCTGAATGTC 1608

RESULT 11

PCT-US94-10487-12

Sequence 12, Application PC/TUS9410487

GENERAL INFORMATION:

APPLICANT: ICOS Corporation

TITLE OF INVENTION: A Novel G Protein-Coupled Receptor

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10487

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/221,817

FILING DATE: 31 MAR 1994

CLASSIFICATION:

APPLICATION NUMBER: 08/123,932

FILING DATE: 17 SEP 1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Grete E.

REFERENCE/DOCKET NUMBER: 27866/11981

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2204 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 31..1758

PCT-US94-10487-12

Query Match 25.2%; Score 418.2; DB 5; Length 2204;

Best Local Similarity 56.2%; Pred. No. 11e-93;

Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 15 GGCCTGGAACAACCTGATGCAACCGCTTACTGCAAGCCCGAAGCCCTGCACTG 74
 DB 33 GAACTCTGAGAACATCGTGAAGCAAGTGTCTACTCAAGCCCGAAGAGTGGCGGTG 92
 QY 75 GCAAGCAAG--AGCTGACGCGGCGGCGGTGACCTGCGCTCGCGAGG 131
 DB 93 AAATCGAAAGCAAAAGCAAGAAATGGCGGAGATGCTCAAGTCTCCATCATCAGCA 152

132 CTGCGGAGCTCCGCAAGAGCTGTCCCTGAACTTCCACAGCTGTGTGAGAGAGCC 191
153 GTGCGAAGAGCTGGGCTCAGCTCGAGCGTGAATCAAGCTGTGAGAGAGAGCCG 212
192 CATTGAGGCGGCTCTTCCGTAATTCCTTACAGAGGCGGAGCTTCCGAGAGGCGC 251
213 CATTGAGGCGGCTCTTCCGTAATTCCTTACAGAGGCGGAGCTTCCGAGAGGCGC 272
252 AACCTTCTAGAGAGCTGCAAGAGCTGAGAGGCGGAGAGGAGAGCCACCAAGAG 311
273 CGCTTCTGATGAGGAGTGGCGAGATGAGAGTACCCGAGATGAGAGGAGAGAGC 332
312 CGGCTGAGAGGAGCTGAGGAGCTTGTGAGAGTGCCTTCCGAGAGAGCCGAGAG 371
333 TGGGAGGAGAGCTTAAAGAGATTTTCTGAGAGAGAGGAGTCTGAGCTTCCGAG 389
372 CTTCCTGAGAGGAGCTGAGAGCTGAGAGGAGAGAGAGAGAGAGAGAGAGT 431
390 GGTGCGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
432 GGTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
449 ACCTTTCCAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
492 GGAATTCGAG 551
507 CGATCTCTGAG 566
552 ACCAGTCTGAG 611
567 GCGAGTGAAG 626
612 GGTATGTCGAG 671
627 GGTGAG 686
672 GAG 731
687 AAG 746
732 GAG 791
747 GAG 806
792 CTGCTGTCGAG 851
807 GTGCTGTCGAG 866
867 CAG 926
912 GCTGAG 971
927 GAG 986
972 GATGAG 1031
987 GATGAG 1046
1032 CAG 1091
1047 CAG 1103
1092 AAG 1151
1104 GATGAG 1163
1152 GATGAG 1211
1164 GATGAG 1223
1212 GAG 1271

1224 GCGCTGTGAG 1283
1272 AGATATTTGAG 1331
1284 ACTTTGCTGAG 1343
1332 GTCTGATGAG 1391
1344 TGCCCGGAG 1403
1392 TGCGCTGATGAG 1451
1404 TGCGAGTGTGAG 1463
1452 TGAATTTGATGAG 1511
1464 GAGATTTGAG 1523
1512 CTTCAG 1571
1524 CTACAG 1583
1572 GCGAGCTTTGAG 1596
1584 CGAGTGTCTTCAG 1608

RESULT 12
US-08-221-817-21
Sequence 21, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoeft, Merle F.
TITLE OF INVENTION: A No. 5532151 G Protein-Coupled Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 13..1740
 US-08-221-817-21

Query Match 23.9%; Score 395.8; DB 1; Length 1983;
 Best Local Similarity 55.3%; Pred. No. 3.5e-88;
 Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

QY 15 GGCCTGGAACAACCTGATGCGCAACCGCCTTACCTGAGCCCGGAAACCTTGACATG 74
 DB 15 GAGAGTCGAGAACATCTGAGCAACCGGCGCTACTCAAGCCCGGAAAGGTGGTGGCCG 74
 QY 75 CGACAGCAAG--AGCTGCAAGGCGCGCGCTGAGCTGCGCCCTCCCGGAGCTGCAAGG 131
 DB 75 GAATGCTAAAGGCAAGAGCAAGAAATGCGCAATGCTGCAAGTTCCCGCAATCGACCA 134
 QY 132 CTGCGGAGAGCTCCGCAAGAGCTGCTCCCTGAACTTCAACAGCTGTGTGAGCAGAGCC 191
 DB 135 GTGTGAAGAGCTCCGCGCTACCTTGAAGGTGACCTACACAGCTGTGTGAGCTGATGTC 194
 QY 192 CATGCGTGGCGGCTCTTCCGTGACTTCTTACCAAGTCCCAAGTTCGCAAGGCGG 251
 DB 195 CATTTGGGCGCTGTTATATGATGATGCTGCGCTACGAGGCTGAGCTGACCGCTGTAC 254
 QY 252 AACCTTCTAGAGAGAGTGCAGAACTGGAGCTGGCCGAGAGGAGACCCCAACAAACG 311
 DB 255 TGCCTTCTGAGTGGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 314
 QY 312 CGGCTGCAAGGCGCTGCTGCACTTGTGCAAGTGCCTTGGCCCGGAGAAACCGCAAC 371
 DB 315 TGGGCGCTC--GGCTAATGCAAGATTTCTGAGCAGACAGGCTCTTGACTCATCCTGA 371
 QY 372 CTTCCTCAAGCCAGGCGCTGCGCAACAAGTGCAGAGCTCCACCTGAGAGAGAGACT 431
 DB 372 AGTTCCCGGCGAGCTGCTGAGTAC-TGTGCCAGCGGCTAGAGAGAGAGAGAGAG 430
 QY 432 GGTGAGAGAGAGCTGCGCAAGGCTGAGGCGATGCTTCTTGAAGAGAGAGCTTAA 491
 DB 431 ACTTCTTCAAGAGAGCTGACCGGCTGAGCTGAGTACCTGAGTGAAGTGGG--CCTTTGG 488
 QY 492 GGAATTCGTAACAGCGCTTCTTACAGCAAGTTCCTGAGTGAAGTGAAGTGAAGTGA 551
 DB 489 CGACTACCTCGACAGAGCTTACTTACACGCTTCTGAGTGAAGTGAAGTGAAGTGA 548
 QY 552 ACCAGTGCAGCAAGTACTTCACTGAGTGAAGTGTGAGGAGAAAGGTGGTTTGGGGA 611
 DB 549 GCGAGTGAACAAAACCTTTAGGAGTGAAGTGTGAGTGAAGTGTGAGTGAAGTGA 608
 QY 612 GGTATGTCGCTGCAAGGTGAAGAAAGCACTGGAGAGATGTGCTGTGAAGAACTGAGCA 671
 DB 609 GGTGTGTGCTGCGAGAGTGAAGCAACAGGAGAGATGTGCTGAAGAACTGAGAA 668
 QY 672 GAAAGGCGCTGAAGAAAGTGTGAGAGAGATGCTCTTCTGAAAGAGAACTTGTGA 731
 DB 669 GAAAGCAATTAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
 QY 732 GAAAGTGCAGAGCGCTTCACTTGTCTCTGAGGCTTGTGCTTGAAGCAAGCCATCT 791
 DB 729 GAAAGTGAACAGTGTGTGTGTATCTTACCTGAGTGAAGTGAAGTGAAGTGAAGTGA 788
 QY 792 CTGCGCTTGTGATGAGCTGATGATGAGGAGAGAGCTCAAGTTCACATCTGAGAGTGG 851
 DB 789 GTGCTGTGTGATGATGATGATGAGGAGAGAGCTCAAGTTCACATCTGAGAGTGG 848
 QY 852 CAAGCGTGTGCTGAGCAATGAGCGGATATCTTTACTGCGCCGAGTACCTGTGAGAT 911
 DB 849 CAAGGCTGTGCTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
 QY 912 GCTGCACTCATTAAGTGTGAGTGTGTATGAGGAGATGAAGCTTGAAGATGTGCTT 971
 DB 909 GAGGAGCTTACACCGGAGAGAGAGTGTGTATGAGGAGAGCTTAAAGCAGAGATATCTTCT 968

QY 972 GATGACCTGCGCACTGAGATTTATCTGACTTGGGCTGGCGCTGAGATGAAGGTGG 1031
 DB 969 GATGACCAATGAGCAATTCGATTCGACCTGGGCTGCTGTGATGTTCTGAGAGG 1028
 QY 1032 CAAGCCATCAACAGAGGCTGGAACCAATGTTTACATGAGCTCTGAGATCTTAATGA 1091
 DB 1029 CCAAGCAATTAAGGCGCTGTGGGCACTGTGGCTACATGAGCTCGAAG--GTGTGA 1085
 QY 1092 AAAGTAAATTAATCTATCTCTGAGAGCTGTTTCCATGAGTGAAGATTAATGAAT 1151
 DB 1086 GATGAGCGCTACATTCAGTCTGAGCTGTGGGAGGCTAGAGCTCTCTTACAGAT 1145
 QY 1152 GTTGTGAGCAACCACTTCAAGATTAAGAAAGTGAAGAAAGTGAAGAGATCTGA 1211
 DB 1146 GATTTGGGAGCAAGTGTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
 QY 1212 GCAAGAACTGTGCAAGAGAGAGTCAAAATTCAGAGATGATTAATCTTCAAGAGAGAG 1271
 DB 1206 GCGGCTGTGAG 1265
 QY 1272 AGATATTGCAAGGCTCTTCTTGTGTAAGAAACAGAGCAAGCTTGAAGAGAGAG 1331
 DB 1266 ACTCTGTTCTCAGCTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
 QY 1332 GTCTGATGATCCAGAGAAACATCTTTTAAACATCACTTCTGCTGAGAGC 1391
 DB 1326 TGCCGTAAGTAAAG 1385
 QY 1392 TGCCCTAATTGAACCCCATTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1451
 DB 1386 TGGAATCTGAAG 1445
 QY 1452 TGAATGATGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1511
 DB 1446 GGAATTAAG 1505
 QY 1512 CTTCAGAACTTTGAG 1571
 DB 1506 CTACAG 1565
 QY 1572 GGAAGTGTGAG 1596
 DB 1566 TGAAGTCTTCAAG 1590

RESULT 13
 US-08-454-439-21
 : Sequence 21, Application US/08454439
 : Patent No. 5591618
 : GENERAL INFORMATION:
 : APPLICANT: Chantry, David
 : APPLICANT: Gray, Patrick W.
 : APPLICANT: Hoekstra, Merle F.
 : TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
 : TITLE OF INVENTION: Kinase GRK6
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 : ADDRESSEE: Borun
 : STREET: 6300 Sears Tower, 233 South Wacker Drive
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: USA
 : ZIP: 60606
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/454,439
 : FILING DATE: 30-MAY-1995

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 559161band, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
US-08-454-439-21

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Query Match 23.9%; Score 395.8; DB 1; Length 1983;

Best Local Similarity 55.3%; Pred. No. 3.5e-88;

Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

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QY 15 GGCCTTGACAACTGATGCGCAACACCGGCTACCTGACAGCGCCGGAAGCCCTCGAGCTG 74
DB 15 GAGAGCTCGAAGACATGCTGAGCGAAGCGGGGCTACCTCAAGCGCCGGGAAGTGTGGGG 74
QY 75 CGACGCAAG--AGCTGACGGCGCGGCGCTGACCTGCGCCCTGCCGGGCTGAGGG 131
DB 75 GATGCTAAAGGCAAGCAAGAAATGCGCGCAGATGCTGAGTCCCGCACATCAGCA 134
QY 132 CTGGCGGAGGCTCGGCCAGAGCTGTCCCTGAACTTCCAGCCGCTGAGCAGAGCC 191
DB 135 GTGTGAGAGCTCCGGCTGACCTTGAAAGTGAACACCAACCTGCTGTAGAGTCAATC 194
QY 192 CATCGATCGCGCTCTTCCGCTGACTTCTAGCCAGACAGTCCAGCTTCGCAAGGCGGC 251
DB 195 CATGGGCGCTGTTATATGATGATCTGCGGTAGAGGCGCTGAGCGTCAACCGGCTGAC 254
QY 252 AACCTTCTAGAGAGTGTGCAAACTGGAGCTGGCCGAGGAGGAGCCACCAAGACAG 311
DB 255 TGCTTCTGATGGGCTGCTGATGATGAGTGAACCCCTGATGAGAAAGGAGCAATG 314
QY 312 CGGCTGAGAGGGGCTGGTGCGCACTTGTGGAGTGGCCCTGCCCCGGGGAACCCGCAAC 371
DB 315 TGGGGGCTC--GGCTAATGAGAAATTTTCTGAGCAACAGGGTCTTGAATCTCAATCC 371
QY 372 CTTCCTCAGCAGGCGCTGGCCACCAAGATGCAAGAGCCACCACTGAGAGAGAGAGT 431
DB 372 AGTTCCTCGGAGCTGGTGTAGTAC--TGTGCCAGGGGCTTAAAGAGAGAGCCCTGAAAG 430
QY 432 GAGTGAATGAGCTGTGCGAAGCTGAGAGCCATGGCTTTCTTGAAGAGAGCCCTTTAA 491
DB 431 ACCTCTTCAGAGAGCTGACCCGCTGAGCCCATGAGTACCTTAAGCATGAGTGGC--CTTTTGG 488
QY 492 GGAATTTGAGACAGGCGCTTCTGAGCAAGATTTCTGAGTGAAGAACTTTGAGATGA 551
DB 489 CGACTACCTCGACAGCACTTACTTCAACCGTTTCTGAGTGAAGAGTGGCTGAGAAAGCA 548
QY 552 ACCAGTGTCAAGCAAGTACTTCACTGAGTTCAGAGTGTCTGGGAAAGGTGATTTTGGGGA 611
DB 549 GCCAGTGAACAAAGAACCTTTTAAAGAGTACCGAGTCTCTGGGCAAAAGGTGGCTTTGGGGA 608
QY 612 GGTATGTGCTTCCAGGTGAAAGAACCTGGGAAATGTATGGCTGTAAAGAACTTGACAA 671

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DB 609 GGTGTGCTCTGCCAGAGGTGGCGCAACAGCGCAAGATGTATGCTTCAAAAACCTGAAAAA 668
QY 672 GAAGCGGCTGAGAAAGAAAGAGTGGCGAAGAGTGGCTCTTGGAAAAGAAATCTTGA 731
DB 669 GAAGCAATTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 728
QY 732 GAAGGTCAAGAGCCCTTTCATGTCTCTCTGAGCTTATGCTTGGAGCAAGACCATCT 791
DB 729 GAAAGTGAACAGTATGATGTATGATCTTATGAGCTTATGAGCAATGAGCAAGATGACCT 788
QY 792 CTGCTTGTGATGAGAGCTTGAATGAGGAGAGAGCTTGAATTCACATCTCAACCTGGG 851
DB 789 GTGCTGTGTGTGATGATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 848
QY 852 CAGCGGTGGCTTGAACATGAGCCGGGTGATCTTTATCTGCGCCAGATAGCTGTGGAGT 911
DB 849 CAGGCTGGCTTTTCCCAAGCAAGTGTCTGTGTCTATGCTGCGGAGATCTGTGTGTCT 908
QY 912 GCTGCACTTCATGAACTCGGATCTGTATCGGAGCATGAAAGCTGAGAAATGTCTTCT 971
DB 909 GAGAGACTTACACCGGAGAGCATGTGTGACAGGAGCTTAAAGCCAGAGATATCTTCT 968
QY 972 GATGACCTCGGCAATGCAAGTATCTGACCTGGGCTGGCCGTGGAGATGAGAGGTGG 1031
DB 969 GATGACCAATGCGCAATTCGAAATCTCGACCTGGGCTGGGCTGTGCAATGTTCTTGA 1028
QY 1032 CAAGCCATCACCCAGAGGCTGGAACCAATGTTATCATGAGCTCTGAGATCTTATGGA 1091
DB 1029 CCAAGCAATCAAAAGGCGGTGTGGGCACTGTGGGCTATCATGAGCTTCCAGAG--GTGGTGA 1085
QY 1092 AAAGTGAATTTATCTATCTCTGTGATCTGTTGCAATGGGATGCAAGATTTATGAAT 1151
DB 1086 GAATGAGCCCTTCAATTCAGTCTGACTGAGTGGGCGCTGAGCTCTCTGTCGAGAT 1145
QY 1152 GCTTGTGAGCAACAAACATTTCAAGAAATTAACAAGAAAGTGTAGTAAAGAGATCTGAA 1211
DB 1146 GATTGGGAGAGTGGCCCTTCAAGCAAGAGAAAGAAATTAAGCGGAGAGGTGGA 1205
QY 1212 GCAAGAACTCTGCAAGAGAGGTCAATTTCCAGCATGATTAATTTCAAGAGAGAGCAA 1271
DB 1206 GCGGCTGTCAAGAGAGGTGTGTGATGAGATGACAGACCGGCTTCCCAAGGAGAGCTC 1265
QY 1272 AGATATTTCAAGGCTCTTCTTGGCTTAAAGAACAGAGCAAGCTTATGAGAGAGAAAA 1331
DB 1266 ACTGTGTCTCAGCTTCTCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1325
QY 1332 GTCTGATGATCCCAAGAGAAATCATTTCTTAAAGAGATGAATTTCTTCCCTGGAAGC 1391
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QY 1392 TGACTAATTTGAACCCCATTTGTGCGAGACCTTCAAGTGTATATGCAAGAGATCGC 1451
DB 1386 TGAATGTCTGAACAACATTTTAAACCTGACCCCAAGGCAATTTATGAGAGAGAGTGT 1445
QY 1452 TGAATTTGATATTTCTGTAGGCTTGGGGGGGTGGAATTTGATGACAAAGTAAAGCTT 1511
DB 1446 GGAATTTGAAGAGTCTTCAAGTAAAGTGTGATCTGAGAGCCCAAGCAAGCAAGCTT 1505
QY 1512 CTGAAAACCTTTGGAAGGTGTCTTCTATAGCAAGGAGAGAGAAATTTATGAAG 1571
DB 1506 CTACAGAGAGTTTGCAGAGGTGTGTGTCTTCAATCCCTTGGCAAGAGAGTGTGAGAGC 1565
QY 1572 GGGAGCTGTTGAGAACTGATGAC 1596
DB 1566 TGAATGCTTCAAGAGAACTAATATGC 1590

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RESULT 14
PCT-US94-10487-21
; Sequence 21, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor

```

TITLE OF INVENTION: Kinase GRK6
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSER: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/10487
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/221,817
 FILING DATE: 31 MAR 1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/123,932
 FILING DATE: 17 SEP 1993
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1983 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 13..1740
 PCT-US94-10487-21

Query Match 23.9%; Score 395.8; DB 5; Length 1983;
 Best Local Similarity 55.3%; Pred. No. 3.5e-88;
 Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

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QY 15 GGCCCTGGCAACCTGATGCGCCCAACGCGCTACCTGACAGCGCGGAAAGCCCTCGGACATG 74
DB 15 GAGGCTCGAAGAACTGTCAGCAACACGCGGCTACCTGAAAGCCCGGAAAGGTGCTGCGG 74
QY 75 CGACAGCAAG--AGCTGACAGCGCGCGCGCTGAGCTGCGCTGCGCGCGCTGACAGG 131
DB 75 GAATGTAAGGCAAGGAGCAAGAAATGCGCGCAAGATGCTGCAAGTCCGCCACATACGCA 134
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DB 135 GTGTAAAGAGCTCGCGCTCACTTGAACGTGACACAGCCCTGTGTAGAGCTCAGTC 194
QY 192 CATCGGTGCGCGCTCTTCGATGATCTTACAGCAACAGTGGCCAGTTCGCAAGCGCG 251
DB 195 CATGGGCGCTGTATATATGATGATCTTGGCTGACAGAGCTGAGCTGACCGCTGAC 254
QY 252 AACCTTCTAGAGAGCTGACAACTGAGAGCTGCGCGAGAGGAGCCCAAGAAAGAG 311
DB 255 TGCCTTCTGAGTGGGCTGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 314
QY 312 CGCGCTGACAGGAGCTGAGTCACTTGTGAGTGTGCGCTGCGCGCGGAGAACCGGCAAC 371
  
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DB 315 TGCGGCTC---GGCTATGACAAATTTTCTGAGGCCACAGCGGTCTGACCTGATCCCTGA 371
QY 372 CTTCCTAGCGCAGGCGCTGCGCCACCAAGTGTGCCAAGAGCCCACTGAGAGAAAGCGAGT 431
DB 372 AGTTCCTCCGCACTGAGTGTGAGTAAAC-TGTGCGCAGCGCTGAGCAGGAGACCTTCGAAAG 430
QY 432 GCGTCAGTACAGCTGCGCAGAGCGTGAAGCCATGAGCTTCTTCGTAAGACAGACCTTTAA 491
DB 431 ACCTTCTCCAGAGAGCTGACCGCGTGAACCAAGATGATCTTAAGATAGGCG--CTTTTGG 488
QY 492 GGAATTTGTACACAGCGCTTCTACAGCAAGTTTCTGACATGAGAACTCTTGAGATGCA 551
DB 489 GACACTACCTGACAGACATCTACTTAACCGTTTCTTGACATGAGAGTGGCTGAAAGGCA 548
QY 552 ACCAGTGTACAGCAAGTACTTCACTGATGATGAGTGTGCGGAAAGTGTGTTGGGGA 611
DB 549 GCAGTACCAAAAACACCTTTAGGCGATACCGAATCTCGGCGCAAGGTGGCTTTGGGGA 608
QY 612 GGTATGTGCGCTGACAGTGAATAAACACTGGGAAAGATGATGCTGTAGAAACCTGACAA 671
DB 609 GGTGTGTGCTGCGCAGGTGCGGACACAGGCAAGATGATGCTGACAAACCTGGAATAA 668
QY 672 GAAGCGGCTGAAGAAAGAAAGGTGCGAGAAATGCTCTCTTGAAGAAAGAAATCTTGA 731
DB 669 GAAACGAATTAAGAAAGCGAAGGGGAGGCGCATGTCTTCAAGAGAAACAGATCTTGA 728
QY 732 GAAGTACAGACCTTCTTCACTGTCTCTGCGCTATGCTCTTGAAGAGAACCATCT 791
DB 729 GAAAGTAAACATGATGATTTGATGATCTTACCTACCATGATGACCAAGATGACAT 788
QY 792 CTGCGCTGTGATGACCTGATGATGAGGAGAGACCTCAAGTCCACATCTACAGTGGG 851
DB 789 GTGCTGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 852 CAGCGGTGCTGAGCATGACATGACCGGCTGATCTTTACTGCGCCAGATGACCTGTGGAT 911
DB 849 CAGGCTGCTGCTTCCGAAAGCAGTCTGTGTTATGCTGCGAGATGCTGTGTGCT 908
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QY 972 GATGACCTGCGCAACTGAGGTTATCTGACCTGAGGCTGCGCGCTGAGATGAAAGGTG 1031
DB 969 GATGACATGAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
QY 1032 CAAGCCATGACCCAGAGGCTGGAACCAATGCTTATGATGCTGAGATCTTATGGA 1091
DB 1029 CCAAGCCATGAAAGGCGCTGAGGCTGATGAGGCTTACATGCTTCCAGAG--GTGCTGAA 1085
QY 1092 AAAGTATGATTTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1151
DB 1086 GATGACGCTGACATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1145
QY 1152 GGTGCTGAGCAAGCAATTCATTAAGATTAACAGAAAGGATGATGATGATGATGAT 1211
DB 1146 GATGCGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1205
QY 1212 GCAAGAACTCTGCAAGACAGGCTCAATTCAGATGATGATGATGATGATGATGATGAT 1271
DB 1206 GCGGCTGCTCAAGAGGCTGATGAGATGATGATGATGATGATGATGATGATGATGAT 1265
QY 1272 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1331
DB 1266 ACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325
QY 1332 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391
DB 1326 TGCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
QY 1392 TGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1451
DB 1386 TGGAATGCTTAAACCACTTTTAAACCTGACCCCGAGCATTTTACTGAGAGAGCTGT 1445
  
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Db 1161 GATCGAGGCCAGTGGCTTCCAGCAGAGAGAGATCAAGCGGAGAGGTGGA 1220
QY 1212 GCAAGAACTCTGCAAGACGAGGTCAATTCAGCATGATTACTTCAAGAGAGCAAA 1271
Db 1221 GCGGCTGTGAAGAGGTCCCGAGAGATTTCCAGCGCTTTCCCGCAGCGCTC 1280
QY 1272 AGATATTTCAGAGCTCTTCTGCTAAGAAACAGAGCAACGCTTAGAGAGAGAGAAA 1331
Db 1281 ACTTTGCTCAGAGTCTCTCTGCAAGAGACCTGCCGAACGACCTGGGGTGTCTGGGG 1340
QY 1332 GTCTG--ATGATCCAGAGAACATCATTTCTTAAAGATCAAATTCTGCTGGA 1388
Db 1341 CAGTGCCTCGAGAGTGAAGAGCACCCCCTTTAAGAGCTGAATTCAAGCGCTGGG 1400
QY 1389 AGCTGGCTTAATTGAACCCCATTTGTGCAAGCTTCAAGTGTATATGCCAAAGACAT 1448
Db 1401 AGCTGGCATGCTGAGAGCGCGTTCAAGCTGAGCCCGAGGCCATTACTGCAAGGATGT 1460
QY 1449 CGCTGAATTGATGATTTCTGTGAGGTTCCGGGGGTGSAATTGATGACAAAGATAAGCA 1508
Db 1461 TCTGACATTGAGAGTCTCTAAGGTCAAGGGGTGAGCTGAGCCTACCGACAGGA 1520
QY 1509 GTTCTTCAAAAATTGCGACAGGTGCTGTCTATAGCATGCGAGAGAAATTATAGA 1568
Db 1521 CTTCTACAGAGATTGCGACAGGCGAGTGTCCATCCCTGCGAGAACGAGATGTGGA 1580
QY 1569 AAGCG 1573
Db 1581 GACCG 1585

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